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RESULT 17
US-10-060-895A-864
; Sequence 864, Application US/10060895A
; Publication No. US20010104401A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN TGF- $\beta$ 1/USO1/00666
; FILE REFERENCE: PB0158
; CURRENT APPLICATION NUMBER: US/10/060,895A
; PRIORITY FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/964,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/315,984
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ. ID NOS: 1582
; SOFTWARE: Acemica Sequence Listing Engine
; SEQ. ID NO 864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-895A-864

Query Match      55.2%; Score 13.8; DB 15; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 1, Conservative 0, Mismatches 2, Indels 0, Gaps 0,
CY      8 TCTATGCTGTGTGTG 24
DB      2 TCAAGCTGTGTGTG 18

RESULT 18
US-10-060-895A-865
; Sequence 865, Application US/10060895A
; Publication No. US20010104401A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN TGF- $\beta$ 1/USO1/00666
; FILE REFERENCE: PB0158
; CURRENT APPLICATION NUMBER: US/10/060,895A
; PRIORITY FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/964,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/315,984
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ. ID NOS: 1582
; SOFTWARE: Acemica Sequence Listing Engine
; SEQ. ID NO 864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-895A-865

Query Match      55.2%; Score 13.8; DB 15; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 1, Conservative 0, Mismatches 2, Indels 0, Gaps 0,
CY      8 TCTATGCTGTGTGTG 24
DB      2 TCAAGCTGTGTGTG 18

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/315,984
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ. ID NOS: 1682
; SOFTWARE: Acemica Sequence Listing Engine
; SEQ. ID NO 865
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-895A-865

Query Match      55.2%; Score 13.8; DB 15; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0,
CY      8 TCTATGCTGTGTGTG 24
DB      1 TCAAGCTGTGTGTG 17

RESULT 19
US-10-098-263B-15996/C
; Sequence 15996, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIORITY FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ. ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ. ID NO 15996
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-263B-15996

Query Match      55.2%; Score 13.8; DB 15; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0,
CY      3 TTTTCTATGCTGTGTG 19
DB      25 TTTGCTATGCTGTGTG 9

RESULT 20
US-09-770-693-19
; Sequence 19, Application US/09770693
; Patent No. US20020069441A1
; GENERAL INFORMATION:
; APPLICANT: Beer, Steven V.
; APPLICANT: Bauer, David W.
; TITLE OF INVENTION: COMPOSITE PEPTIDE FRAGMENT (PANDININ II) BY ACTION OF
; TITLE OF INVENTION: EMBODIMENT: INHIBITOR EXPRESSION OF A HETEROLOGOUS
; FILE REFERENCE: 19603/2501
; CURRENT APPLICATION NUMBER: US/09/770,693
; PRIORITY FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,065
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ. ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 19

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LENGTH: 32  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: primer  
 US-09-770-693-19

Query Match 55.4% Score 13.6 DB 15 Length 32  
 Best Local Similarity 89.0% Pred No 1 (e+04)  
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

Db 1  
 1 TTTCTTCTATAGCTGCTT 20  
 20 TTTCTTCTATAGCTGCTT 1

RESULT 21  
 US-09-830-133-10  
 Sequence 1: Artificial Sequence  
 Publication No: US2002024590A1  
 GENERAL INFORMATION:  
 APPLICANT: 3e Rivercity, Therese  
 APPLICANT: Semlaud, Florian  
 TITLE OF INVENTION: Data Theory With Directed Disaggregation  
 FILE REFERENCE: 01/03 154 75/03/25,413  
 CURRENT FILING DATE: 2001 04 17  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: Patent version 2.1  
 SEQ ID NO 10  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Data Theory  
 OTHER INFORMATION: Data Theory With Directed Disaggregation  
 US-09-841-439-10

Query Match 54.4% Score 13.6 DB 15 Length 25  
 Best Local Similarity 89.0% Pred No 1 (e+04)  
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

Db 1  
 1 TTTCTTCTATAGCTGCTT 20  
 20 TTTCTTCTATAGCTGCTT 22

RESULT 22  
 US-10-215-112-475-0  
 Sequence 4755: Application US/10215112  
 Publication No: US2003004256A1  
 GENERAL INFORMATION:  
 APPLICANT: Michael Mittman  
 TITLE OF INVENTION: Methods of Sequencing Analysis of Nucleic  
 FILE REFERENCE: 2003  
 CURRENT FILING DATE: 2002 09 09  
 NUMBER OF SEQ ID NOS: 10036  
 SOFTWARE: Feature: For Windows Version 4.0  
 SEQ ID NO 4755  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Data Theory  
 US-10-215-112-4755

Query Match 54.4% Score 13.6 DB 15 Length 25  
 Best Local Similarity 89.0% Pred No 1 (e+04)  
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

Query 1 TTTCTTCTATAGCTGCTT 20  
 Db 20 TTTCTTCTATAGCTGCTT 1

RESULT 23  
 US-10-098-263B-19017  
 Sequence 19017: Artificial Sequence  
 Publication No: US2003019410A1  
 GENERAL INFORMATION:  
 APPLICANT: Mittman, Michael  
 TITLE OF INVENTION: Human Microarray  
 FILE REFERENCE: 3118.1  
 CURRENT FILING DATE: 2003-01-08  
 PRICE APPLICATION NUMBER: 02/025,179  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 13106  
 SOFTWARE: Microarray File Software Listing Generator V 1.1  
 SEQ ID NO 19017  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Data Theory  
 US-10-098-263B-19017

Query Match 54.4% Score 13.6 DB 15 Length 25  
 Best Local Similarity 89.0% Pred No 1 (e+04)  
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

Db 5  
 5 TTTCTTCTATAGCTGCTT 24  
 24 TTTCTTCTATAGCTGCTT 24

RESULT 24  
 US-10-098-263B-19018  
 Sequence 19018: Artificial Sequence  
 Publication No: US2003019410A1  
 GENERAL INFORMATION:  
 APPLICANT: Mittman, Michael  
 TITLE OF INVENTION: Human Microarray  
 FILE REFERENCE: 3118.1  
 CURRENT FILING DATE: 2003-01-08  
 PRICE APPLICATION NUMBER: 02/025,179  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 13106  
 SOFTWARE: Microarray File Software Listing Generator V 1.1  
 SEQ ID NO 19018  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Data Theory  
 US-10-098-263B-19018

Query Match 54.4% Score 13.6 DB 15 Length 25  
 Best Local Similarity 89.0% Pred No 1 (e+04)  
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

Db 5  
 5 TTTCTTCTATAGCTGCTT 24  
 24 TTTCTTCTATAGCTGCTT 24

RESULT 25  
 US-10-098-263B-19047-0  
 Sequence 19047: Application US/10098263B  
 Publication No: US2003019410A1  
 GENERAL INFORMATION:  
 APPLICANT: Mittman, Michael  
 TITLE OF INVENTION: Human Microarray  
 FILE REFERENCE: 3118.1  
 CURRENT FILING DATE: 2003-01-08  
 PRICE APPLICATION NUMBER: 02/025,179  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 13106  
 SOFTWARE: Microarray File Software Listing Generator V 1.1  
 SEQ ID NO 19047  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Data Theory  
 US-10-098-263B-19047-0



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: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: IBM PC COMPATIBLE
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1 TCTATGTCCTTGGT 1





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APPLICANT: Zhang, Jian  
APPLICANT: Gu, Yizhong  
APPLICANT: "Jingye" Cui-Tuog  
APPLICANT: HONG, JIE  
APPLICANT: HONG, JIE

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FILE REFERENCE: PB0158
: CURRENT APPLICATION NUMBER: US/16/060,895A
: CURRENT FILING DATE: 2002-06-10
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 09/864,761
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/315,984
: PRIOR FILING DATE: 2001-08-30
: NUMBER OF SEQ ID NOS: 1682
: SOFTWARE: A-omics Sequence Listing Engine
: SEQ ID NO 856
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Homo sapiens
US 10-060-895A.856

Query Match      51.2%; Score 12.8; DB 15; Length 25;
Best local Similarity 87.5%; Pctd No 149+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY      8 TCTATGCTGCTGTGGT 23
      ||| ||||| |||||
Db      10 TCAAGTGTGCTGTGGT 25
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Search completed: July 21, 2003, 18:30:43  
Job time : 69.3942 secs



GenCore version 5.1.6  
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OM nucleic acid search, using sw model

Run on: July 21, 2003, 12:47, Search time: 641.467 seconds  
(without alignments)  
641.100 Million cell updates/sec

Title: US-09-890-363-6

Perfect score: 25

Sequence: 1 tttcttttctatgtgtgtgtgtga g

Scoring table: 16164066 seqs, 80074376 residues

Total number of hits satisfying the search parameters: 45420

Minimum DB seq length: 0  
Maximum DB seq length: 35

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database:

EST:  
1: em\_estha.\*  
2: em\_esthuma.\*  
3: em\_estini.\*  
4: em\_estinu.\*  
5: em\_estov.\*  
6: em\_estp1.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: qb\_est1.\*  
10: qb\_est2.\*  
11: qb\_hic.\*  
12: qb\_est3.\*  
13: qb\_est4.\*  
14: qb\_est5.\*  
15: em\_estfun.\*  
16: em\_estcom.\*  
17: qb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_huv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_tod.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	57.6	38	17	A2630154
2	14.4	57.6	33	17	A2635403
3	14.2	56.8	31	17	AA969179
4	13.9	55.2	30	17	A2747322
5	13.9	55.2	35	17	A2774652
6	13.6	54.4	31	9	AI364767

7	13.6	54.4	33	17	A2630154
8	13.4	53.6	25	9	A1495770
9	13.4	53.6	25	9	A1495770
10	13.4	53.6	34	14	B93052
11	13.2	52.8	34	14	A1419301
12	13.2	52.8	19	17	A2868350
13	13.2	52.8	22	17	A2868350
14	13.2	52.8	34	14	CO1136
15	13.2	52.8	22	17	A2868350
16	13.2	52.8	22	17	A2868350
17	13.2	52.8	22	17	A2868350
18	13.2	52.8	22	17	A2868350
19	13.2	52.8	22	17	A2868350
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75	13.2	52.8	22	17	A2868350
76	13.2	52.8	22	17	A2868350
77	13.2	52.8	22	17	A2868350
78	13.2	52.8	22	17	A2868350
79	13.2	52.8	22	17	A2868350

[illegible]





372	10.4	40.8	34	1	AD00677	AD00677	410	10	37	32	17	EM01306	EM01306
373	10.4	40.8	34	1	AD00678	AD00678	410	10	37	32	17	EM01307	EM01307
374	10.4	40.8	34	1	AD00679	AD00679	410	10	37	32	17	EM01308	EM01308
375	10.4	40.8	34	1	AD00680	AD00680	410	10	37	32	17	EM01309	EM01309
376	10.4	40.8	34	1	AD00681	AD00681	410	10	37	32	17	EM01310	EM01310
377	10.4	40.8	34	1	AD00682	AD00682	410	10	37	32	17	EM01311	EM01311
378	10.4	40.8	34	1	AD00683	AD00683	410	10	37	32	17	EM01312	EM01312
379	10.4	40.8	34	1	AD00684	AD00684	410	10	37	32	17	EM01313	EM01313
380	10.4	40.8	34	1	AD00685	AD00685	410	10	37	32	17	EM01314	EM01314
381	10.4	40.8	34	1	AD00686	AD00686	410	10	37	32	17	EM01315	EM01315
382	10.4	40.8	34	1	AD00687	AD00687	410	10	37	32	17	EM01316	EM01316
383	10.4	40.8	34	1	AD00688	AD00688	410	10	37	32	17	EM01317	EM01317
384	10.4	40.8	34	1	AD00689	AD00689	410	10	37	32	17	EM01318	EM01318
385	10.4	40.8	34	1	AD00690	AD00690	410	10	37	32	17	EM01319	EM01319
386	10.4	40.8	34	1	AD00691	AD00691	410	10	37	32	17	EM01320	EM01320
387	10.4	40.8	34	1	AD00692	AD00692	410	10	37	32	17	EM01321	EM01321
388	10.4	40.8	34	1	AD00693	AD00693	410	10	37	32	17	EM01322	EM01322
389	10.4	40.8	34	1	AD00694	AD00694	410	10	37	32	17	EM01323	EM01323
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[illegible]





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ALIGNMENTS

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., St. UT  
 84112, USA  
 Tel. 801 585 6606  
 Fax. 801 585 7177  
 Email: [jung@polymers.utah.edu](mailto:jung@polymers.utah.edu)  
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 Laboratory mouse colony.  
 The DNA  
 was hydrolytically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with 14 DNA polymerases and 14  
 polynucleotide kinase. Adapter oligonucleotides were  
 ligated to the blunt ends in high salt buffers. The  
 ligated DNA was purified and a 26 nucleotide 1st a 3rd to  
 adapted DNA using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of FMD4 (19147-19149) (GenBank:U03220105115). The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted vector DNA was ligated to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli X110-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

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TITLE	24 bp	mus	1000	1000	1000
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COMMENT	24 bp	mus	1000	1000	1000

RESULT 2  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
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 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

IMAF conservant microfag. In good for further information.  
Trace considered overall poor quality

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/db_xref="taxon.10030"

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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="vector: pMD22v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passages through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (3'-1473211430/412972.1), a copy-number indelible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 19 a 6 c 2 g 3 t  
 Query Match 55.2% Score 13.5; Pz 17; Length 10;  
 Best Local Similarity 98.2% Pz 17; Gz 10;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCTTTCTATGCTGCT 17  
 18 TTTCTTTCTATGCTGCT 2

RESULT 5  
 AC136467  
 DEFINITION: Mouse 10kb plasmid UUCGM library Mus musculus genomic clone UUCGM00004111 F. PNA sequence  
 AC136467.1 31 bp CNA linear GSS 16 FEB-2001  
 AC136467.1 31:12900155  
 GSS:  
 house mouse  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 31)  
 Bunin, D., Aoyagi, A., Barber, M., Pearson, T., Duval, E., Hamill, J., Islam, H., Longacre, S., Mahmoud, M., Meenon, E., Pedersen, T., Reilly, M., Rose, M., Rose, P., Stokes, P., Tinney, A., von Niederhausen, A., and Wright, D., Weiss, P.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert P. Weiss  
 UNIVERSITY OF UTAH Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S 2000 P., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunham@genetics.utah.edu  
 Insert Length: 10000 bp Error: 0.00  
 Plate: 0004 Row: 1 Column: 11  
 Seq primer AGTTCTAAACGACGACGACCT  
 Class: plasmid ends  
 High quality sequence stop: 35.  
 Location/Qualifiers  
 1..35  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCGM00004111"

/clone\_lib="Mouse 10kb plasmid UUCGM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="vector: pMD22v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passages through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (3'-1473211430/412972.1), a copy-number indelible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 17 a 6 c 6 g 6 t  
 Query Match 55.2% Score 13.9; Pz 17; Length 35;  
 Best Local Similarity 97.8% Pz 17; Gz 10;  
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTTCTTTCTATGCTGCTGCTGCTGA 25  
 33 TTTCTTTCTATGCTGCTGCTGCTGA 9

RESULT 6  
 A1364767/c  
 1000s  
 DEFINITION: Human 31 bp mRNA linear EST 07-JAN-1999  
 A1364767.1 31:10241 NCT CGAG CAGC Homo sapiens cDNA clone IMAGE1965123 3' similar to TR-033563 Q33563 EATPO 144 PDB/PODBST, data sequenced  
 A1364767  
 A1364767.1 31:4124456  
 EST.  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 31)  
 NCI-CCRP http://www.ncbi.nlm.nih.gov/ncicrp.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgs@femail.nih.gov  
 Tissue procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA library preparation: Life Technologies, Inc.  
 cDNA library arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI CGAP clone distribution information can be found through the L.V.A.G.E. Consortium/LNC at:  
 www.bio.illn.gov/dbp/image/image.html

FEATURES  
 SOURCE  
 1..31  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1965123"  
 /clone\_lib="NCI CGAP C723"  
 /issue\_type="mRNA", 5' pooled (see description)"  
 /lab\_host="DH10B"









purified. The sheared, adaptered mouse DNA was annealed to adaptered vector DNA, and transformed into chemically competent E. coli XL10 and plated on LB agar and selected for ampicillin resistance."

## BASE COUNT

0 a 4 c 5 g 13 t

Query Match 52.8% Score 13.2 DP 17 Length 22  
Best Local Similarity 83.3% Pred. No. 9.5e+05  
Matches 15, Conservative 0, Mismatches 7, Indels 0, Gaps 0

## CY

1 TTTCTTTCTATGCTGCT 19  
2 TTTCTTTCTATGCTGCT 20  
3 TTTCTTTCTATGCTGCT 20

## RESULT 13

COL136/c

DOCS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COL136/c Human adult fibroblast RNA  
Sequence  
Accession  
Version  
Keywords  
Source  
Organism  
Reference  
Authors  
Title  
Journal  
Comment  
Human  
Human sapiens  
Eukaryotic; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo  
1 (bases 1 to 24)  
Osaka, K.  
BodyMap: human gene expression database  
Unpublished (1995)  
Contact: Osaka, K.  
Institute for Molecular and Cellular Biol  
Osaka University  
1-3, Yamadaoka, Suita, Osaka Pref. 565, Japan  
Tel: 06-877-5111 (ex.3315)  
Email: kouekus@mol.mol.osaka-u.ac.jp  
Human gene signature, 3'-directed cDNA sequence. We are not submitting the same cDNA sequence information. We have not  
For the abundance information of clones with this sequence in this  
library and as well as in other 3'-directed libraries, see  
http://www.fdb.mol.mol.osaka-u.ac.jp/3prime/ The sequence of the clones  
represented by this 3' sequence is also found there.  
Location/Qualifiers  
1..34  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human adult (KOsaka)"  
/dev\_stage="adult"

## FEATURES

Source

## BASE COUNT

22 a 4 c 2 g 5 t 1 others

## ORIGIN

Query Match 52.8% Score 13.2 DP 17 Length 22  
Best Local Similarity 83.3% Pred. No. 9.5e+05  
Matches 15, Conservative 0, Mismatches 7, Indels 0, Gaps 0

## CY

1 TTTCTTTCTATGCTGCT 19  
2 TTTCTTTCTATGCTGCT 20  
3 TTTCTTTCTATGCTGCT 20

## Db

33 TTTCTTTCTATGCTGCT 15

## RESULT 14

AA999803  
Accession  
Version  
Keywords  
Source  
Organism  
Reference  
Authors  
Title  
Journal  
Comment  
Human  
Human sapiens  
Eukaryotic; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo  
1 (bases 1 to 22)  
NCI CCRF, http://www.ncbi.nlm.nih.gov/nciccrf  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: rstraus@nci.nih.gov  
Research Program: NCI/Christopher Mochlyuk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CGAP Library Preparation: M. Bento Soares, Ph.D.  
CGAP Library Arrived by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI CGAP clone distribution information can be  
found through the T.M.A.G.E. Consortium/URL at:  
www.bic.mcgill.gov/hyp/image/image.html

## BASE COUNT

0 a 1 c 4 g 17 t

Query Match 52.8% Score 13.2 DP 17 Length 22  
Best Local Similarity 83.3% Pred. No. 9.5e+05  
Matches 15, Conservative 0, Mismatches 7, Indels 0, Gaps 0

## CY

1 TTTCTTTCTATGCTGCT 21  
2 TTTCTTTCTATGCTGCT 21  
3 TTTCTTTCTATGCTGCT 21

## RESULT 15

AA912788/c

DOCS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA912788/c Human adult fibroblast RNA  
Sequence  
Accession  
Version  
Keywords  
Source  
Organism  
Reference  
Authors  
Title  
Journal  
Comment  
Human  
Human sapiens  
Eukaryotic; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo  
1 (bases 1 to 22)  
NCI CCRF, http://www.ncbi.nlm.nih.gov/nciccrf  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: rstraus@nci.nih.gov  
Research Program: NCI/Christopher Mochlyuk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CGAP Library Preparation: M. Bento Soares, Ph.D.  
CGAP Library Arrived by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI CGAP clone distribution information can be  
found through the T.M.A.G.E. Consortium/URL at:  
www.bic.mcgill.gov/hyp/image/image.html

## FEATURES

Source

## BASE COUNT

22 a 1 c 4 g 17 t

## ORIGIN

Query Match 52.8% Score 13.2 DP 17 Length 22  
Best Local Similarity 83.3% Pred. No. 9.5e+05  
Matches 15, Conservative 0, Mismatches 7, Indels 0, Gaps 0

## CY

1 TTTCTTTCTATGCTGCT 21  
2 TTTCTTTCTATGCTGCT 21  
3 TTTCTTTCTATGCTGCT 21

## Db

1 TTTCTTTCTATGCTGCT 21

## RESULT 15

REFERENCE 1 (bases 1 to 25)

AUTHORS NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute Cancer Genome Anatomy Project (CGAP).

JOURNAL Tumor Gene Index

COMMENT Unpublished (1997)

Contact: Robert Straussberg, Ph.D.

Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

This clone is available directly from the NIH, contact the

IMAGE Consortium (info@imga.nih.gov) for further information.

Trace considered overall poor quality

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence strip: 1

#### FEATURES

source

1..25

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGF1525060"

/clone\_lib="Soares\_NFL\_T\_GBC\_S1"

/lab\_host="DH10B"

/note="Organism pooled. Vector: pTZ19-Tag (Pharmacia) with

a modified polylinker site. Not 1, Site 2, Eco RI,

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung Nbl10W, testis NHT, and B-cell

NCI CGAP GCB1) were mixed, and ss circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones with

from the same 3 libraries. The pools consisted of

1. M.A.G.B. clones 79740, 79741, 79742, 79743, 79744, 79745,

72608-72871, and 72906-73109. Subtraction by Benne

Soares and M. Fatima Bonaldi. "

#### BASE COUNT

19 a 2 c 2 g 2 t

#### ORIGIN

Query Match 52.0% Score 13, PB 9, Length 25,

Best Local Similarity 76.0% Fwd No. 1 Rev No. 1

Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

21 TTTTCTTCTATCTCTCTTCTG 21

21 TTTTCTTCTATCTCTCTTCTG 4

RESULT 16

AZ442116

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

RM. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunne@genetics.utah.edu](mailto:ddunne@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

#### FEATURES

source

1..26

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UG51M24508"

/clone\_lib="Mouse 10kb plasmid U99GM library"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, 10 resistant, 4"

/note="Vector: pMD420, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

<http://www.jax.org/> and Dr. J. A. Rothman. The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adapter oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (31473114.9b) (AF129922.1), a copy number

unstable derivative of plasmid p1. The vector was ligated

with adapters complementary to the short adapters and

purified. The sheared, adapted mouse DNA was annealed to

adapter vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

#### BASE COUNT

6 a 3 c 6 g 11 t

#### ORIGIN

Query Match 52.0% Score 13, PB 17, Length 26,

Best Local Similarity 76.0% Fwd No. 1 Rev No. 1

Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

5 TTTTCTATCTCTCTTCTGTA 25

6 TTTTCTTCTCTCTCTCTTCTG 26

RESULT 17

AZ596498

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

RM. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunne@genetics.utah.edu](mailto:ddunne@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00









Db 1 TTCTTTTGTGTGTGGGCTGG 22

RESULT 24  
D19580/c 25 bp mRNA linear EST 12 DEC 1995  
LOCUS M585000987 Mouse 3'-directed Mus musculus domesticus cDNA clone  
DEFINITION mb1684 3', mRNA sequence.  
ACCESSION D19580  
VERSION D19580.1 GI:1089439  
KEYWORDS EST.  
SOURCE western European house mouse.  
ORGANISM Mus musculus domesticus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sinothamnini; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
AUTHORS Kawamura, S., Orita, Y., Yoshida, T., Katsuki, M. and Matsubara, K.  
TITLE Analysis of gene expression in mouse embryogenesis by 3' directed  
cDNA sequencing  
JOURNAL: Nucleic Acids Res. 21, 4978-4983, 1993  
COMMENT Copyright 1995, Orita, Y., Yoshida, T., Katsuki, M. and Matsubara, K.  
Institute for Cellular and Molecular Biology  
Osaka University  
3-1 Yamadaoka, Suita, Osaka 565, Japan.  
FEATURES  
source  
1..25  
Location/Qualifiers  
/organism="Mus musculus domesticus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10092"  
/clone\_lib="mb1684"  
/clone\_lib="Mouse 3'-directed"  
/tissue\_type="fetal tissue (day 6.5-8.5 of gestation)"

BASE COUNT 18 a 3 c 3 g 1 t

ORIGIN

Query Match 49.6% Score 12.4; E-14; Length 25;  
Best Local Similarity 72.7% Freq No. 1.7e+06;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTTCTTTCTATGTCGCTGG 22  
DB 25 TTCTTTTCTTTTCTTTGG 4

RESULT 25  
AA867596 28 bp mRNA linear EST 16 MAR 1998  
LOCUS AA867596/c  
DEFINITION clone IMAGE:1294298 5' similar to TR:Q33563 Q33563 EATRO 164  
K12902FAST, cDNA sequence.  
ACCESSION AA867596  
VERSION AA867596.1 GI:12961041  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sinothamnini; Muridae; Murinae; Mus.  
1 (bases 1 to 28)  
AUTHORS Marra, M., Hillier, L., Allen, M., Powell, M., Dietrich, N., Duhon, T.,  
Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Scholtenberg, K., Shapiro, M., Tan, F., Underwood, J., Moore, B.,  
Theisinger, R., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 9501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through NCBI, and at the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:675346  
Trace considered overall poor quality  
Possible reversed clone; similarity on wrong strand  
Seq primer: 28mb1 rev1 ET from Amerham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..28  
/organism="Mus musculus"  
/db\_xref="taxon:10092"  
/clone\_lib="IMAGE:1294298"  
/clone\_lib="Stratagene mouse macrophage (#91746)"  
/tissue\_type="macrophage"  
/dev\_stage="MEH1-3 cell line"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Oligo 11bp, Vector: pGEMT2 (DE 2 Site 1)  
ESCR1, Site 2, XhoI, Cloned directionality: 5' primer:  
Oligo dt, MEH1-3 cell line, Averago insert size: 1.5 kb;  
Uni ZAP XR Vector, -5' adapter sequence: 5'-GAGATGTTTCTTTTCTTTT  
3'-3' adapter sequence: 5'-GAGATGTTTCTTTTCTTTT 4"

BASE COUNT 17 a 4 c 4 g 3 t

ORIGIN

Query Match 49.6% Score 12.4; E-14; Length 28;  
Best Local Similarity 72.7% Freq No. 1.7e+06;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TTCTTTTCTATGTCGCTGG 23  
DB 22 TTCTTTTCTATGTCGCTGG 1

RESULT 26  
A1623404/c 28 bp mRNA linear EST 14 DEC 1995  
LOCUS A1623404  
DEFINITION cDNA7 x1 NCI CGAP 14 HMG sequence cDNA 1 to 28 MAR 22 1998  
Similar to sw1004\_PASTE ribov9 HYPOHEILAM 14 kb to PROTEIN 1  
mRNA sequence.  
ACCESSION A1623404  
VERSION A1623404.1 GI:4648335  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 28)  
AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap/  
National Cancer Institute, Cancer Cell Line Project (CCRLP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
Tissue Procurement: Christopher Munkittrick, M.D., Ph.D., Michael P.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Fred Lammert, Ph.D.  
cDNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the NCBI M.A.G.E. Consortium (http://www.ncbi.nlm.nih.gov/mage/mage.html)

JOURNAL COMMENT

FEATURES  
source  
1..28  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:2230548"  
/clone\_lib="NCI CGAP:14"



**AUTHORS**  
Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, R., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meegen, E., Peterson, T., Reilly, M., Rose, M., Rose, P., Stokes, P., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.

**TITLE**  
Mouse whole genome scaffolding with paired and reads from 10kb plasmid inserts

**JOURNAL**  
Unpublished (2000)

**COMMENT**  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 104, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: rdumegenetics@utah.edu  
Insert Length: 10000 seq Error: 0.00  
Plate: 0136 row: 5 column: 13  
Seq primer: CACACATCAAACTGCTATCAAT  
class: plasmid ends  
High quality sequence stop: 32.  
Location/Qualifiers  
1..32  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGCM0116113"  
/clone\_lib="Mouse 10kb Plasmid UUCGCM library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD2019, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dares/). The DNA was hydrolytically sheared by repeated passage through a 0.008 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. After 24 h ligations with ligated to the blunt ends in high molar excess. The adaptered RNA was purified and size-selected for 4.9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector RNA was prepared from a derivative of pMD20 (G14732114G14732072.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adapters complementary to the insert adapters and purified. The sheared, adaptered mouse DNA was annealed to adaptered vector RNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**BASE COUNT**  
4 a 5 c 6 g 17 t

**ORIGIN**  
Query Match 49.6%, Score 12.4, DB 17, Length 32;  
Best Local Similarity 72.7%, Pred. NO. 1.7e+06;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

**QY**  
1 TTTTCTTCTATGCTGCTG3 22  
|||||  
6 TTTATTTCATCAAAATTC3 27

**Db**

**RESULT 30**  
AM250918 33 bp mRNA linear EST 07 JAN 2000  
LOCUS  
DEFINITION  
283153 RefSeq NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:283153 3', mRNA sequence.  
VERSION  
AM250918  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 33)

**AUTHORS**  
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

**TITLE**  
Other ESTs: 282153.5prime

**JOURNAL**  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov

**COMMENT**  
Tissue Procurement: DCTD/DPB cDNA Library Preparation Unit  
Regev/Podh Laboratory cDNA Library Arrayed by The I.M.A.G.E. Consortium (UMD) RNA Sequencing by Perlegen MGC sequencing project clone distribution. MGC clone distribution information can be found through the I.M.A.G.E. Consortium/UMD at: <http://www.bio.umd.edu/bioproj/umc/umc.html>  
Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross-match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: [http://www.genome.washington.edu/low\\_quality/sequence/19](http://www.genome.washington.edu/low_quality/sequence/19)  
Notes: This high quality trace followed vector sequencing. Very low quality sequence: trace file contained 33 contiguous distinct peaks following vector sequence. Polyadenylation based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate L1C06 row: 5 column: 2  
High quality sequence stop: 19.  
Location/Qualifiers  
1..33  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821153"  
/clone\_lib="NIH MGC 7"  
/tissue\_type="Small Cell Carcinoma"  
/cell\_line="M203"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organism: Human, Vector: pMD2019, Size: 19 XhoI Site: 283153, cDNA made by oligo dT priming. Internationally cloned into EcoRI/XbaI sites with the following adapter: GGCACACAGC. cDNA selected length for average insert size 1.8kb. Library constructed by Ann Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

**BASE COUNT**  
6 a 5 g 19 t

**ORIGIN**  
Query Match 49.6%, Score 12.4, DB 10, Length 33;  
Best Local Similarity 72.7%, Pred. NO. 1.7e+06;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

**QY**  
1 TTTCTTCTATGCTGCTG3 22  
|||||  
3 TTTTTCATCAAAATTC3 24

**Db**

**RESULT 31**  
AZ597662 34 bp DNA linear GSS 14 DEC 1999  
LOCUS  
DEFINITION  
1M4111P19 M. musculus 130001 cDNA library, M. musculus, 130001, cDNA sequence.  
VERSION  
AZ597662  
KEYWORDS  
GSS.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Rodentia; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 34)  
Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, R., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meegen, E., Peterson, T., Reilly, M., Rose, M., Rose, P., Stokes, P., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts



FEATURES at <http://www.sanger.ac.uk/ftp/genomes/11001/>  
Location/Qualifiers

## SOURCE

1.330  
/organism="Trypanosoma brucei"  
/strain="TPE0927"  
/db\_xref="taxon:5691"  
/clone="119b02"

BASE COUNT 7 a 6 c 7 g 10 t  
ORIGIN

Query Match 48 88; Score 12.2; DB 13; Length 33;  
Best Local Similarity 82 48; Pval No 1 9e+06;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 CTATCTCTCTCTCTGA 25  
|||||  
Db 12 CTATGAGCTGTGTGTA 28

RESULT 34  
R0046766/c 33 bp mRNA 11001 EST 07 DEC 2001  
LOCUS R0046766 R0046766 N19B Mochii normalized Xenopus neurula library Xenopus  
DEFINITION laevis cDNA clone X1014924 3', mRNA sequence.  
ACCESSION R0046766 GI:17406013  
VERSION R0046766  
KEYWORDS EST.  
SOURCE African clawed frog.  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
Xenopodinae; Xenopus.  
1 (bases 1 to 33)  
AUTHORS Kitayama, A., Toratsuka, C., Mochii, M., Taniguchi, N., Shin-I, T. and Kohata  
Y.

## REFERENCE

Expressed genes in X laevis oocyte.  
Submitted (2001)  
Contact: Tadashi Shin-I  
Center for Genetic Research Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tsunagi@nig.ac.jp.  
Location/Qualifiers

1.33  
/organism="Xenopus laevis"  
/db\_xref="taxon:9355"  
/clone="X014924"  
/clone\_lib="N19B Mochii normalized Xenopus neurula  
library"  
/tissue\_type="whole embryo"  
/dev\_stage="stage 15"  
/cset="vstage: FRSP3, Stage 1 Mat 1, Stage 2, Eosin, COMAS  
were cloned, purified and differentially cloned. Stage  
according to Mischak and Fabel library is subcloned  
and was constructed by N. Taniguchi and A.M. Tori,  
(Wellcome/CRC Institute)"

BASE COUNT 20 a 4 c 5 g 4 t  
ORIGIN

Query Match 48 88; Score 12.2; DB 13; Length 33;  
Best Local Similarity 82 48; Pval No 1 9e+06;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTCAATGCTGTGTGA 25  
|||||  
Db 32 TTTTCTTTTCTTCTTCTGTA 8

RESULT 35  
AV834098/c 35 bp mRNA linear EST 09 MAY 2002  
LOCUS AV834098

## DEFINITION

AV834098 cDNA library: Hordern vulgare subsp. vulgare  
vulgare short germination Hordern vulgare subsp. vulgare cDNA  
clone bags409, mRNA sequence.

## ACCESSION

AV834098  
AV834098 1 GI:14526187  
EST.

## VERSION

EST.

## KEYWORDS

EST.

## SOURCE

EST.

## ORGANISM

EST.

## REFERENCE

Hordern vulgare subsp. vulgare.  
Hordern vulgare subsp. vulgare.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
Triticeae; Hordeum.  
1 (bases 1 to 35)  
Sato, K.

## JOURNAL

Barley EST sequencing project in NIG and Okayama Univ  
Unpublished (2001)  
Contact: Kazuhito Sato  
Research Institute for Bioreresources  
Okayama University, Barley Germplasm Center  
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan  
Email: kazatosato@okayama-u.ac.jp,  
URL: <http://www.rib.okayama-u.ac.jp/barley/>  
database: <http://www.silva.rdg.ac.uk/rib/barley/>  
Location/Qualifiers

1.35  
/organism="Hordeum vulgare subsp. vulgare"  
/cultivar="Haruna Nijo"  
/db\_xref="taxon:112509"  
/clone="bags409"  
/clone\_lib="K. Sato unpublished cDNA library: Hordeum  
vulgare subsp. vulgare short germination"  
/tissue\_type="shoots"  
/dev\_stage="germination"

BASE COUNT 24 a 3 c 2 g 6 t  
ORIGIN

Query Match 48 88; Score 12.2; DB 10; Length 33;  
Best Local Similarity 82 48; Pval No 1 9e+06;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTCAATGCTGTGTGA 25  
|||||  
Db 28 TTTTCTTTTCTTCTTCTGTA 4

RESULT 36  
AA911173/c 42 bp mRNA linear EST 09 JUN 1998  
LOCUS AA911173 c881310 s1 NCI-CGAP K343 Homo sapiens cDNA clone IMAGE1526146 3'

## DEFINITION

similar to TR-04192 5'3192 NAB1 LETHYNOGENASE GENE  
sequence.  
AA911173  
AA911173.1 GI:3050463  
EST.

## ACCESSION

AA911173  
AA911173 1 GI:3050463  
EST.

## VERSION

EST.

## KEYWORDS

EST.

## SOURCE

EST.

## ORGANISM

EST.

## REFERENCE

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eulalia, Primates, Catarrhini, Hominoidea, Homo.  
1 (bases 1 to 22)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/UMI at:  
[www.bio.lnh.gov/bhrp/image/image.html](http://www.bio.lnh.gov/bhrp/image/image.html)

## JOURNAL

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/UMI at:  
[www.bio.lnh.gov/bhrp/image/image.html](http://www.bio.lnh.gov/bhrp/image/image.html)

## TITLE

Tumor Gene Index  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

## COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/UMI at:  
[www.bio.lnh.gov/bhrp/image/image.html](http://www.bio.lnh.gov/bhrp/image/image.html)











US-10-000-835A-95A  
Sequence 95A Application US/7060895A  
Publication No. US2003014407A1  
GENERAL INFORMATION:  
CLASSIFICATION

[illegible]

RESULT 12  
 US-10-060-895A-859  
 Sequence 859, Application US/10060895A  
 Application No. US20030104403A1  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Jian  
 APPLICANT: Gu, Yinhong  
 APPLICANT: Nguyen, Trung  
 TITLE OF INVENTION: HUMAN UDP-GALNA4 POLYPEPTIDE N ACETYLGLUCOSAMINE TRANSFERASE 10  
 TITLE REFERENCE: PB0158  
 CURRENT APPLICATION NUMBER: US/10/060,895A  
 CORRESPONDING APPLICATION NUMBER: US/03/01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/03064  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: -30  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663

[illegible][illegible]

PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/006658  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/006658  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/006658  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 09/864,761  
 PRIOR FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/315,994  
 PRIOR FILING DATE: 2001-09-19  
 NUMBER OF SEQ ID NOS: 1682  
 SOFTWARE: Acemica Sequence Listing Engine  
 SEQ ID NO: 88  
 LENGTH: 17  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-060-895A-88

Query Match 55.2%; Score 13.8; DB 15; Length 17;  
 Best Local Similarity 89.2%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 8 TCTATGCTGCTGCTG 24  
 1 TCAAGTCTGCTGCTG 17

RESULT 8  
 US-09-918-156 14/c  
 Sequence 14, Application US/09318156  
 Publication No. US20030104403A1  
 GENERAL INFORMATION:  
 APPLICANT: Hanany, Francis  
 APPLICANT: Lubin, Matthew  
 TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING  
 TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES  
 FILE REFERENCE: 19603/441  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US 09/245,156  
 PRIOR FILING DATE: 2001-01-30  
 NUMBER OF SEQ ID NOS: 76  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO: 34  
 LENGTH: 21  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence  
 OTHER INFORMATION: oligonucleotide sequence  
 US-09-918-156 14

Query Match 55.2%; Score 13.8; DB 12; Length 21;  
 Best Local Similarity 89.2%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 2 TCTATGCTGCTGCTG 18  
 18 TCTATGCTGCTGCTG 2

RESULT 9  
 US-09-918-156 14/c  
 Sequence 16, Application US/0918156  
 Publication No. US20030104403A1  
 GENERAL INFORMATION:  
 APPLICANT: Hanany, Francis  
 APPLICANT: Lubin, Matthew  
 TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING  
 TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES  
 FILE REFERENCE: 19603/441  
 CURRENT APPLICATION NUMBER: US/0918156

CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/918,156  
 PRIOR FILING DATE: 2001-01-30  
 NUMBER OF SEQ ID NOS: 76  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO: 36  
 LENGTH: 21  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:  
 OTHER INFORMATION: oligonucleotide sequence  
 US-09-918-156 36

Query Match 55.2%; Score 13.8; DB 12; Length 21;  
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 2 TCTATGCTGCTGCTG 18  
 18 TCTATGCTGCTGCTG 2

RESULT 10  
 US-10-060-895A-857  
 Sequence 857, Application US/10060895A  
 Publication No. US20030104403A1  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Jian  
 APPLICANT: Gu, Yizhong  
 TITLE OF INVENTION: HUMAN CDR3 SALVAGE POLYMERIZATION  
 FILE REFERENCE: PB0158  
 CURRENT APPLICATION NUMBER: US/10/060,895A  
 CURRENT FILING DATE: 2002-06-10  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00673  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 09/864,761  
 PRIOR FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/315,984  
 PRIOR FILING DATE: 2001-08-30  
 NUMBER OF SEQ ID NOS: 1603  
 SOFTWARE: Acemica Sequence Listing Engine  
 SEQ ID NO: 857  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-060-895A-857

Query Match 55.2%; Score 13.8; DB 15; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 8 TCTATGCTGCTGCTG 24  
 18 TCAAGTCTGCTGCTG 25

RESULT 11



```

C 966 10.4 41.6 25 15 US-10-098-263B-21191 Sequence 21191, A
967 10.4 41.6 25 15 US-10-098-263B-22226 Sequence 22226, A
968 10.4 41.6 25 15 US-10-098-263B-24628 Sequence 24628, A
969 10.4 41.6 25 15 US-10-098-263B-27021 Sequence 27021, A
970 10.4 41.6 25 15 US-10-098-263B-29427 Sequence 29427, A
971 10.4 41.6 25 15 US-10-098-263B-31432 Sequence 31432, A
972 10.4 41.6 25 15 US-10-098-263B-33837 Sequence 33837, A
973 10.4 41.6 25 15 US-10-098-263B-36242 Sequence 36242, A
974 10.4 41.6 25 15 US-10-098-263B-38648 Sequence 38648, A
975 10.4 41.6 25 15 US-10-098-263B-41144 Sequence 41144, A
976 10.4 41.6 25 15 US-10-098-263B-43413 Sequence 43413, A
977 10.4 41.6 25 15 US-10-098-263B-45817 Sequence 45817, A
978 10.4 41.6 25 15 US-10-098-263B-48223 Sequence 48223, A
979 10.4 41.6 25 15 US-10-098-263B-50627 Sequence 50627, A
980 10.4 41.6 25 15 US-10-098-263B-53033 Sequence 53033, A
981 10.4 41.6 25 15 US-10-098-263B-55439 Sequence 55439, A
982 10.4 41.6 25 15 US-10-098-263B-57844 Sequence 57844, A
983 10.4 41.6 25 15 US-10-098-263B-60249 Sequence 60249, A
984 10.4 41.6 25 15 US-10-098-263B-62654 Sequence 62654, A
985 10.4 41.6 25 15 US-10-098-263B-65059 Sequence 65059, A
986 10.4 41.6 25 15 US-10-098-263B-67464 Sequence 67464, A
987 10.4 41.6 25 15 US-10-098-263B-69869 Sequence 69869, A
988 10.4 41.6 25 15 US-10-098-263B-72274 Sequence 72274, A
989 10.4 41.6 25 15 US-10-098-263B-74679 Sequence 74679, A
990 10.4 41.6 25 15 US-10-098-263B-77084 Sequence 77084, A
991 10.4 41.6 25 15 US-10-098-263B-79489 Sequence 79489, A
992 10.4 41.6 25 15 US-10-098-263B-81894 Sequence 81894, A
993 10.4 41.6 25 15 US-10-098-263B-84299 Sequence 84299, A
994 10.4 41.6 25 15 US-10-098-263B-86704 Sequence 86704, A
995 10.4 41.6 25 15 US-10-098-263B-89109 Sequence 89109, A
996 10.4 41.6 25 15 US-10-098-263B-91514 Sequence 91514, A
997 10.4 41.6 25 15 US-10-098-263B-93919 Sequence 93919, A
998 10.4 41.6 25 15 US-10-098-263B-96324 Sequence 96324, A
999 10.4 41.6 25 15 US-10-098-263B-98729 Sequence 98729, A
1000 10.4 41.6 25 15 US-10-098-263B-101134 Sequence 101134, A

```

## ALIGNMENTS

## RESULT 1

```

US-10-098-263B-7164
/ Sequence 7164, Application US/10098263B
/ Publication No. US20020010441A1
/ GENERAL INFORMATION:
/ APPLICANT: Millman, Michael
/ TITLE OF INVENTION: HUMAN MICRORNA
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098-263B
/ CURRENT FILING DATE: 2003-01-09
/ PRIORITY APPLICATION NUMBER: 60/220,759
/ PRIORITY FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 7164
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-098-263B-7164

```

```

Query Match 50.4%, Score 15.6, DB 15, Length 25,
Best Local Similarity 81.8%, Pred. No. 2.4e+03,
Matches 18, Conservative 0, Mismatches 4, Indels 0, Gaps 0

```

```

CY 2 TTTTTCATGCTGCTGCT 23
|||||
DB 4 TTTTTCATGCTGCTGCT 25
|||||

```

## RESULT 2

```

US-10-098-263B-720
/ Sequence 720, Application US/10098263B
/ Publication No. US20020010441A1
/ GENERAL INFORMATION:
/ APPLICANT: Millman, Michael
/ TITLE OF INVENTION: HUMAN MICRORNA
/ FILE REFERENCE: 3118.1

```

```

/ GENERAL INFORMATION:
/ APPLICANT: EDELMAN, IENA
/ APPLICANT: JACOBSON, ETHERNE DANIEL, FRANCOIS
/ APPLICANT: BRIAND, JEAN-PAUL
/ TITLE OF INVENTION: HEMATOPOIETIC MOLECULES CONTAINING A WITTING AGENT TO TARGET
/ TITLE OF INVENTION: SPECIFIC CELLS AND A MOLECULE REGULATING THE APPEARANCE
/ TITLE OF INVENTION: PRODUCTION OF THE PERMEABILITY TRANSITION FROM COMPLEX
/ TITLE OF INVENTION: (PPTP)
/ FILE REFERENCE: 01445,0216
/ CURRENT APPLICATION NUMBER: US/10/098-263B
/ CURRENT FILING DATE: 2002-09-29
/ PRIORITY APPLICATION NUMBER: 60/265,194
/ PRIORITY FILING DATE: 2001-02-02
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patent In War 2.1
/ SEQ ID NO 260
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE: Description of Artificial Sequence: Protein
US-10-098-263B-720

```

## Query Match

```

Best Local Similarity 84.2%, Score 14.7, DB 15, Length 30,
Matches 16, Conservative 3, Mismatches 3, Indels 0, Gaps 0

```

```

CY 7 TTTTTCATGCTGCTGCTGCT 25
|||||
DB 6 TTTTTCATGCTGCTGCTGCT 24
|||||

```

## RESULT 3

```

US-09-801-274-740
/ Sequence 740, Application US/09801274
/ Patent No. US20020032119A1
/ GENERAL INFORMATION:
/ APPLICANT: Landey, Eric S.
/ APPLICANT: Ireland, James S.
/ TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
/ FILE REFERENCE: 2825,2002-001
/ CURRENT APPLICATION NUMBER: US/09/801-274
/ CURRENT FILING DATE: 2001-03-07
/ PRIORITY APPLICATION NUMBER: US 60/197,510
/ PRIORITY FILING DATE: 2000-03-07
/ NUMBER OF SEQ ID NOS: 1802
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 740
/ LENGTH: 31
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-801-274-740

```

```

Query Match 56.8%, Score 14.2, DB 10, Length 31,
Best Local Similarity 76.2%, Pred. No. 9.3e+03,
Matches 16, Conservative 1, Mismatches 4, Indels 0, Gaps 0

```

```

CY 4 TTTTTCATGCTGCTGCTGCT 24
|||||
DB 1 TTTTTCATGCTGCTGCTGCT 21
|||||

```

## RESULT 4

```

US-10-098-263B-7163
/ Sequence 7163, Application US/10098263B
/ Publication No. US20020010441A1
/ GENERAL INFORMATION:
/ APPLICANT: Millman, Michael
/ TITLE OF INVENTION: HUMAN MICRORNA
/ FILE REFERENCE: 3118.1

```









[illegible]





CM nucleic - nucleic search using SW model  
 July 21, 2003, 14:35:32 : Search time 01.2276 seconds  
 (without adjustments)  
 042,750 Million cell updates/score

Searched: 1439767 sec, 100%  
 Parameters: 100%

```

Total time: 0.000000
Minimum DB seq length: 0
Maximum DB seq length: 35
Post-processing: Minimum Match 0%
                    Maximum Match 100%
                    first 1000 summaries

```

Maximum Listing	March first	1008	Summaries
1000			

[illegible]

SUMMARIES

## SUMMARY

Description

Result	DB	Match	Length	ID
1	15.6	b7.4	37	US-10-039-177 7164
2	15.6	b7.4	37	US-10-055-211 740
3	14.2	b6.8	31	US-09-803-274 740
4	14.2	b6.8	31	US-10-098-967-7163
5	14	b6.0	26	US-08-812-937-21
6	14	b6.0	26	US-09-153-120-48
7	14	b6.0	26	US-09-153-895A-48
8	14	b6.0	17	US-10-060-156-34
9	13.8	b5.2	12	US-07-918-156-36
10	13.8	b5.2	11	US-10-918-156-36
11	13.8	b5.2	11	US-10-918-156-36
12	13.8	b5.2	11	US-10-060-855A-857
13	13.8	b5.2	11	US-10-060-855A-857
14	13.8	b5.2	11	US-10-060-855A-857
15	13.8	b5.2	11	US-10-060-855A-857
16	13.8	b5.2	11	US-10-060-855A-857
17	13.8	b5.2	11	US-10-060-855A-857
18	13.8	b5.2	11	US-10-060-855A-857
19	13.8	b5.2	11	US-10-060-855A-857
20	13.8	b5.2	11	US-10-060-855A-857
21	13.8	b5.2	11	US-10-060-855A-857
22	13.8	b5.2	11	US-10-060-855A-857
23	13.8	b5.2	11	US-10-060-855A-857
24	13.8	b5.2	11	US-10-060-855A-857
25	13.8	b5.2	11	US-10-060-855A-857
26	13.8	b5.2	11	US-10-060-855A-857
27	13.8	b5.2	11	US-10-060-855A-857
28	13.8	b5.2	11	US-10-060-855A-857
29	13.8	b5.2	11	US-10-060-855A-857
30	13.8	b5.2	11	US-10-060-855A-857
31	13.8	b5.2	11	US-10-060-855A-857
32	13.8	b5.2	11	US-10-060-855A-857
33	13.8	b5.2	11	US-10-060-855A-857
34	13.8	b5.2	11	US-10-060-855A-857
35	13.8	b5.2	11	US-10-060-855A-857
36	13.8	b5.2	11	US-10-060-855A-857
37	13.8	b5.2	11	US-10-060-855A-857
38	13.8	b5.2	11	US-10-060-855A-857
39	13.8	b5.2	11	US-10-060-855A-857
40	13.8	b5.2	11	US-10-060-855A-857
41	13.8	b5.2	11	US-10-060-855A-857
42	13.8	b5.2	11	US-10-060-855A-857
43	13.8	b5.2	11	US-10-060-855A-857
44	13.8	b5.2	11	US-10-060-855A-857
45	13.8	b5.2	11	US-10-060-855A-857
46	13.8	b5.2	11	US-10-060-855A-857
47	13.8	b5.2	11	US-10-060-855A-857
48	13.8	b5.2	11	US-10-060-855A-857
49	13.8	b5.2	11	US-10-060-855A-857
50	13.8	b5.2	11	US-10-060-855A-857
51	13.8	b5.2	11	US-10-060-855A-857
52	13.8	b5.2	11	US-10-060-855A-857
53	13.8	b5.2	11	US-10-060-855A-857
54	13.8	b5.2	11	US-10-060-855A-857
55	13.8	b5.2	11	US-10-060-855A-857
56	13.8	b5.2	11	US-10-060-855A-857
57	13.8	b5.2	11	US-10-060-855A-857
58	13.8	b5.2	11	US-10-060-855A-857
59	13.8	b5.2	11	US-10-060-855A-857
60	13.8	b5.2	11	US-10-060-855A-857
61	13.8	b5.2	11	US-10-060-855A-857
62	13.8	b5.2	11	US-10-060-855A-857
63	13.8	b5.2	11	US-10-060-855A-857
64	13.8	b5.2	11	US-10-060-855A-857
65	13.8	b5.2	11	US-10-060-855A-857
66	13.8	b5.2	11	US-10-060-855A-857
67	13.8	b5.2	11	US-10-060-855A-857
68	13.8	b5.2	11	US-10-060-855A-857
69	13.8	b5.2	11	US-10-060-855A-857
7				

[illegible]



Wed Jul 23 09:24:58 2003

us-09-890-363-6.max.mni

QY 2 TTTCTTCTATGCTGTGTTG 22  
Db 5 TTCAGCTCTAGGCTGTGTTG 25

RESULT 39  
US-09-247-190-37  
Sequence 37, Application US/02-247190  
Patent No. 6214549  
GENERAL INFORMATION:  
APPLICANT: Szostak, Jack W.  
APPLICANT: Fawcett, Richard W.  
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN  
FILE REFERENCE: 00786/350005  
CURRENT FILING DATE: US/03/247,190  
CURRENT APPLICATION NUMBER: 60/035,963  
EARLIER FILING DATE: 1999-02-09  
EARLIER APPLICATION NUMBER: 60/064,491  
EARLIER FILING DATE: 1997-11-06  
EARLIER APPLICATION NUMBER: 09/007,005  
EARLIER FILING DATE: 1998-01-14  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DNA splint  
US-09-247-190-37  
Query Match 52.0%; Score 13; DB 4; Length 26;  
Best Local Similarity 72.7%; Pred. No 3.7e+03;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TTTCTTCTATGCTGTGTTG 24  
Db 1 TTTTCTTTTACCTTTGTTG 22

RESULT 40  
US-09-051-079-1  
Sequence 1, Application US/09051079A  
Patent No. 6214549  
GENERAL INFORMATION:  
APPLICANT: WEINDEL, Kurt  
APPLICANT: TASCHNER, Gerhard  
TITLE OF INVENTION: METHOD OF DETECTING A SUBSTANCE TO BE ANALYZED  
FILE REFERENCE: 101614-07096  
CURRENT FILING DATE: US/09/051,079A  
CURRENT APPLICATION NUMBER: PCT/EP96/04358  
EARLIER FILING DATE: 1998-09-10  
EARLIER APPLICATION NUMBER: DE/195 37 952.7  
EARLIER FILING DATE: 1995-10-12  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 1  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc. binding  
LOCATION: (1)-(27)  
OTHER INFORMATION: The nucleotide in position 1 contains biotin  
OTHER INFORMATION: bound the symbol n means a amino acid and labeled with  
OTHER INFORMATION: with 6-amino hexanoic acid and labeled with

OTHER INFORMATION: digoxigenin-N-hydroxy succinimide-ester.  
FEATURE: Description of Artificial Sequence:  
OTHER INFORMATION: oligodeoxynucleotide  
US-09-051-079-1  
Query Match 52.0%; Score 13; DB 4; Length 27;  
Best Local Similarity 69.4%; Pred. No 3.7e+03;  
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TTTCTTCTATGCTGTGTTG 24  
Db 1 TTTTCTTTTACCTTTGTTG 23  
Search completed: July 21, 2003, 15:40:28  
Cpu time: 26.1617 secs

ZIP: 20905  
 COMPUTER READABLE FORM  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,335  
 FILING DATE: 06-JAN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/775,393  
 FILING DATE: 03-JAN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KILL, David J.  
 REGISTRATION NUMBER: 36,576  
 REFERENCE/DOCKET NUMBER: 400000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)628-8800  
 TELEFAX: (202)628-8800  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US 08 779 335 17

Query Match 52.0%, Score 13, DB 3, Length 25,  
 Best Local Similarity 76.2%, Freq. No. 3.7e+03,  
 Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0.

RESULT 17  
 US 08 938 835A-17  
 Sequence 17, Application US/08938835A  
 Patent No. 6060245  
 GENERAL INFORMATION:  
 APPLICANT: SORCE, Joseph A.  
 APPLICANT: WILLIAMS, Rebecca L.  
 TITLE OF INVENTION: METHODS AND MATERIALS FOR GENERATING  
 TITLE OF INVENTION: SPECIFIC NUCLEIC ACID SEQUENCES  
 NUMBER OF SEQUENCES: 62  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fungo, H. H.  
 ADDRESS: Fungo, H. H.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3115  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,335A  
 FILING DATE: 26-SEPT-1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/775,393  
 FILING DATE: 03-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/779,335  
 FILING DATE: 06-JAN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barker, M. Paul

REGISTRATION NUMBER: 32,013  
 REFERENCE/DOCKET NUMBER: 04121 6044 02000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-938-835A-17

Query Match 52.0%, Score 13, DB 3, Length 25,  
 Best Local Similarity 76.2%, Freq. No. 3.7e+03,  
 Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0.

RESULT 38  
 PCT-US94-14096-6  
 Sequence 6, Application PCT/US9414096  
 GENERAL INFORMATION:  
 APPLICANT: NIKIFOROV, THEO  
 APPLICANT: KNAPP, MICHAEL  
 TITLE OF INVENTION: METHOD FOR THE IMMUTILIZATION OF NUCLEIC  
 TITLE OF INVENTION: ACID MOLECULES  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWREY & SIMON  
 STREET: 1299 PENNSYLVANIA AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/14096  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: AUERBACH, JEFFREY I.  
 REGISTRATION NUMBER: 32,680  
 REFERENCE/DOCKET NUMBER: 639-106  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 383-7451  
 TELEFAX: (202) 383-6610  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Equus caballus  
 IMMEDIATE SOURCE:  
 CLONE: 680  
 PCT-US94-14096-6





CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-4415  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 08/779,335  
 FILING DATE: 26 SEPT 1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/775,903  
 FILING DATE: 03 JAN 1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/779,335  
 FILING DATE: 06-JAN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Baker, M. Paul  
 REGISTRATION NUMBER: 32,013  
 REFERENCE/DOCKET NUMBER: 641-1 0044 0000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 30:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08 938 835A 30  
 Query Match: 5.8% Score 13.2, DE 3, Length 20  
 Best Local Similarity: 29.3% Pred No. 3, 0.03  
 Matches: 15; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0  
 4 CTTTCTTCTTCTTCTTCTG 18  
 16 2 CTTATGATGTCCTGCTG 20  
 RESULT 32  
 US-09-036-315-4  
 Sequence 4, Application US/09036315  
 Patent No. 6218523  
 GENERAL INFORMATION:  
 APPLICANT: French, Cynthia K.  
 APPLICANT: Schneider, Patrick A.  
 APPLICANT: Yamamoto, Karen K.  
 TITLE OF INVENTION: Frostbite Lesion Specific Marker  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Potreroadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/036,315  
 FILING DATE: 06 MAR 1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/047,811  
 FILING DATE: 15 MAY 1997

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/041,246  
 FILING DATE: 07 MAR 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Storella, John R.  
 REGISTRATION NUMBER: 22,944  
 REFERENCE/DOCKET NUMBER: 019002 00021015  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 FEATURE:  
 NAME/KEY: -  
 LOCATION: 1-30  
 OTHER INFORMATION: /nuclo- "AT" 01139 (3485) Lower Primer  
 US-09-036-315-4  
 Query Match: 5.8% Score 13.2, DE 4, Length 30  
 Best Local Similarity: 83.3% Pred No. 3, 1e+03  
 Matches: 15; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0  
 1 TTTCTTTCTTCTTCTG 18  
 Db 12 TTTCTTTCTTCTTCTG 29  
 RESULT 33  
 US-08-779-355-4  
 Sequence 4, Application US/08779355  
 Patent No. 6017701  
 GENERAL INFORMATION:  
 APPLICANT: Sauer, Joseph A.  
 APPLICANT: Mullins, Rebecca L.  
 TITLE OF INVENTION: WEIGHT AND ADAPTS FOR GENERATING  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Evenson, McKean, Edwards & Lennihan P.C.  
 STREET: 1200 G Street N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,355  
 FILING DATE: 06-JAN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/775,993  
 FILING DATE: 03-JAN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kulik, David J.  
 REGISTRATION NUMBER: 36,576  
 REFERENCE/DOCKET NUMBER: 43992CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)628-8800  
 TELEFAX: (202)628-8844  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single

REFERENCE/SEQUENCE NUMBER: 2000 1000000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)751-6880  
 TELEFAX: (212)751-6849  
 INFORMATION FOR SEQ ID NO: 101:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 BASE PAIRS  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 US-09-678-437-101  
 Query Match 52.6%, Score 13.2, DB 3, Length 31  
 Best Local Similarity 52.6%, Pval No. 2.0e+03,  
 Matches 15, Conservative 0, Mismatches 5, Indels 0  
 CY 2 TTTCTTCTGATGCTGTTG 74  
 DB 23 TTTCTTCTGATGCTGTTG 1

RESULT 29  
 US-09-072-384-12  
 Sequence 12, Application US/090300004  
 Patent No. 6153420  
 GENERAL INFORMATION:  
 APPLICANT: MILLINAX, JOSEPH A.  
 TITLE OF INVENTION: METHOD FOR GENERATING  
 TITLE OF INVENTION: SPECIFIC NUCLEIC ACID SEQUENCES  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZYMOGENESIS, INC.  
 STREET: 1201 Firstlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTEST FOR Windows Version 1.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/090300004  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARKER, GARY E.  
 REGISTRATION NUMBER: 31,648  
 REFERENCE/SEQUENCE NUMBER: 97-1601  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6673  
 TELEFAX: 206-442-6678  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Other  
 IMMEDIATE SOURCE:  
 CLONE: Z013509  
 US-09-072-384 12

Query Match 52.6%, Score 13.2, DB 3, Length 18  
 Best Local Similarity 52.6%, Pval No. 2.0e+03,  
 Matches 15, Conservative 0, Mismatches 3, Indels 0, Gaps 0

5 TTTCTATGCTGTTG 74  
 DB 23 TTTCTATGCTGTTG 18

RESULT 30  
 US-09-779-355-30  
 Sequence 30, Application US/09079355  
 Patent No. 6017701  
 GENERAL INFORMATION:  
 APPLICANT: SORGE, JOSEPH A.  
 TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING  
 TITLE OF INVENTION: SPECIFIC NUCLEIC ACID SEQUENCES  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: EVERGEN, INCORPORATED, Edwards & Lemahan P.L.L.C.  
 STREET: 1200 G Street N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09079355  
 FILING DATE: 02 JAN 1997  
 CLASSIFICATION: 435  
 INFORMATION FOR SEQ ID NO: 30:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: RNA (Genomic)  
 US-08-779-355-30

Query Match 52.6%, Score 13.2, DB 3, Length 20  
 Best Local Similarity 78.9%, Pval No. 3e+03,  
 Matches 15, Conservative 0, Mismatches 4, Indels 0, Gaps 0

CY 4 TTTCTATGCTGTTG 22  
 DB 2 TTTCTATGCTGTTG 20

RESULT 31  
 US-08-948-945A-40  
 Sequence 40, Application US/08939393A  
 Patent No. 6060245  
 GENERAL INFORMATION:  
 APPLICANT: SORGE, JOSEPH A.  
 TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING  
 TITLE OF INVENTION: SPECIFIC NUCLEIC ACID SEQUENCES  
 NUMBER OF SEQUENCES: 69  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: EVERGEN, INCORPORATED, Edwards & Lemahan P.L.L.C.  
 STREET: 1200 G Street N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN & FINNEGAN  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/068,478  
 FILING DATE: 26 OCT 1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/02908  
 FILING DATE: 29 MAR 1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 34,398  
 FILING DATE: 27 MAR 1992  
 CLASSIFICATION: 435  
 INFORMATION FOR SEQ ID NO. 101:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 BASE PAIRS  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 US-09-890-478-101

Query Match 53.6% Score 13.4; DR 2; Length 11;  
 Best Local Similarity 73.9%; Pred. No. 2.6e+03;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0.

QY 2 TTTCTTTGATGCTGCTGCTG 24  
 TTTCTTTGATGCTGCTGCTG 1

RESULT 27  
 US-09-414-117-101/c  
 Sequence 101, Application US/09/414,117  
 Patent No. 6291664  
 GENERAL INFORMATION:  
 ADDRESSEE: MORGAN & FINNEGAN  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/414,117

FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/850,049  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/02908  
 FILING DATE: 29 MAR 1993  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/858,747  
 FILING DATE: 27 MAR 1992  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MORRY, MARY J.  
 REGISTRATION NUMBER: 34,398  
 REFERENCE/DOCKET NUMBER: 2026 4006US1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)751-6849  
 TELEFAX: (212)751-6849  
 INFORMATION FOR SEQ ID NO. 101:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 BASE PAIRS  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 US-09-414-117-101

Query Match 53.6% Score 13.4; DR 4; Length 11;  
 Best Local Similarity 73.9%; Pred. No. 2.6e+03;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0.

QY 2 TTTCTTTGATGCTGCTGCTG 24  
 TTTCTTTGATGCTGCTGCTG 1

RESULT 28  
 US-09-678-437-101/c  
 Sequence 101, Application US/09/678,437  
 Patent No. 641413  
 GENERAL INFORMATION:  
 ADDRESSEE: MORGAN & FINNEGAN  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/678,437  
 FILING DATE: 02-OCT-2000  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/850,949  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: PCT/US93/02908  
 FILING DATE: 29-MAR-1993  
 APPLICATION NUMBER: US 07/858,747  
 FILING DATE: 27 MAR 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MORRY, MARY J.  
 REGISTRATION NUMBER: 34,398

Wed Jul 23 09:24:58 2003

us-09-890-363-6.max.rml

APPLICANT: Swenson, Jeff  
APPLICANT: Kamb, Alexander  
APPLICANT: Harsman, Keith D.  
APPLICANT: Shattuck-Eidens, Donna M.  
APPLICANT: Livingston, Sean V.  
APPLICANT: Wipman, Kevin W.  
APPLICANT: Pittman, P. Andrew  
TITLE OF INVENTION: Method for Diagnosing a  
TITLE OF INVENTION: Prostatectomy for Breast and Ovarian Cancer  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Hurd & Ciochetti, LLP  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.0  
CURRENT APPLICATION DATA: PCT/US95/10229  
APPLICATION NUMBER: PCT/US95/10229  
FILING DATE:  
CLASSIFICATION:  
PRIORITY INFORMATION DATA:  
APPLICATION NUMBER: US  
FILING DATE: 07-JUN-1995  
PRIORITY INFORMATION DATA: US 08/409,305  
APPLICATION NUMBER: US 08/409,305  
FILING DATE: 24-MAR-1995  
PRIORITY INFORMATION DATA: US 08/348,824  
APPLICATION NUMBER: US 08/348,824  
FILING DATE: 29-NOV-1994  
PRIORITY INFORMATION DATA:  
APPLICATION NUMBER: US 08-304,104  
FILING DATE: 14-SEP-1994  
PRIORITY INFORMATION DATA:  
APPLICATION NUMBER: US 08/300,266  
FILING DATE: 02-SEP-1994  
PRIORITY INFORMATION DATA:  
APPLICATION NUMBER: US 08/283,221  
FILING DATE: 12-AUG-1994  
PRIORITY INFORMATION DATA:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey D., 957  
REGISTRATION NUMBER: 24884-109347  
REFERENCE/AGENT NUMBER: 24884-109347  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8100  
INFORMATION CHARACTERISTICS:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPology: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PCT-US95-10220-71  
Query Match 54.4%; Score 13.6; DB 5; Length 30;  
Best local similarity 80.0%; Pct 3; No 1; Indels 4; Gaps 0;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
DB 1 TTTTTCCTGATGCTGCTG 20  
8 TGTCTTCTGATGCTGCT 27  
RESULT 25

US-08-850-049-101/c  
Sequence 101, Application US/08850049  
Patent No. 5965726  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: METHOD OF ELIMINATING  
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF RNA  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA: US/08/450,043  
APPLICATION NUMBER: US/08/450,043  
FILING DATE: 02-MAY-1997  
CLASSIFICATION: 435  
PRIORITY INFORMATION DATA:  
APPLICATION NUMBER: US 08/050,478  
FILING DATE: 26-OCT-1994  
PRIORITY INFORMATION DATA:  
APPLICATION NUMBER: PCT/US93/02908  
FILING DATE: 29-MAR-1993  
PRIORITY INFORMATION DATA:  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/858,747  
FILING DATE: 27-MAR-1992  
PRIORITY INFORMATION DATA:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MERRY, MARY J.  
REGISTRATION NUMBER: 34,198  
REFERENCE/AGENT NUMBER: 2006-4006051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)751-6849  
INFORMATION FOR SEQ ID NO: 101:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPology: LINEAR  
US-08-850-049-101  
Query Match 53.4%; Score 13.4; DB 2; Length 31;  
Best local similarity 73.3%; Pct 2; No 2; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 2 TTTTTCCTGATGCTGCTG 24  
23 TTTTTCCTGATGCTGCTG 1  
RESULT 26  
US-08-050-478-101/c  
Sequence 101, Application US/08050478  
Patent No. 5972596  
GENERAL INFORMATION:  
APPLICANT:  
APPLICANT:  
APPLICANT:  
TITLE OF INVENTION: METHOD OF ELIMINATING  
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF RNA  
NUMBER OF SEQUENCES: 130

```

STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10203
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07 JUN 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24 MAR 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29 NOV 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/309,104
FILING DATE: 16 SEP 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02 SEP 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/299,221
FILING DATE: 12 AUG 1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihmen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24844-100347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 962 4810
TELEFAX: 202 962 8300
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10203-71

Query Match 54.4%; Score 13.6; DB 5; Length 30;
Best Local Similarity 80.0%; Pctd No 2 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 23  
PCT-US95-10203-71

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Sequence 71, Application PC/TUS9510203
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Hartman, Keith E.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.

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CY 1 TTTCTTTTATATGCTTTT 20
DB 8 TTTCTTTTATATGCTTTT 27

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APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSER: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10203
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07 JUN 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24 MAR 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29 NOV 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/309,104
FILING DATE: 16 SEP 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02 SEP 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/299,221
FILING DATE: 12 AUG 1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihmen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24844-100347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 962 4810
TELEFAX: 202 962 8300
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10203-71

Query Match 54.4%; Score 13.6; DB 5; Length 30;
Best Local Similarity 80.0%; Pctd No 2 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 24

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PCT-US95-10220-71
Sequence 71, Application PC/TUS9510220
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio

```

```

CY 1 TTTCTTTTATATGCTTTT 20
DB 8 TTTCTTTTATATGCTTTT 27

```

Page 15

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-TS/MS-PCS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/040,727  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA: US 08/483,554  
 APPLICATION NUMBER: 07-JUN-1995  
 FILING DATE:  
 PRIOR APPLICATION DATA: US 08/348,824  
 APPLICATION NUMBER: 07-NOV-1994  
 FILING DATE:  
 PRIOR APPLICATION DATA: US 08/309,104  
 APPLICATION NUMBER: 16-SEP-1994  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/300,266  
 FILING DATE: 02 SEP-1994  
 PRIOR APPLICATION DATA: US 08/377,221  
 APPLICATION NUMBER: 11-APR-1994  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24894-1-0347  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-362-4810  
 TELEFAX: 202-362-8400  
 INFORMATION FOR SEQ ID NO: 71:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-08-850-727-71  
 Query Match 54.4% Score 13.6, DB 4, Length 30;  
 Best Local Similarity 80.0%, Ident. No. 2, Ident. 4, Index 0;  
 Matches 16; Conservative 0; Mismatches 4;  
 QY 1 TTCTCTTCTATGCTGCT 20  
 DB 8 TGCTCTTCTATGATCTCT 27  
 RESULT 22  
 PUT-0895-10302-71  
 Sequence 71: Application PC/TUS951022  
 GENERAL INFORMATION:  
 APPLICANT: Shattuck-Bidens, Donna X.  
 APPLICANT: Simard, Jacques  
 APPLICANT: Emi, Mitsuru  
 APPLICANT: Nakamura, Yunsuke  
 APPLICANT: Durocher, in Vivo Mutations and Polymorphisms  
 TITLE OF INVENTION: In the 17q-linked Breast and Ovarian Cancer  
 TITLE OF INVENTION: Susceptibility Gene  
 NUMBER OF SEQUENCES: 85  
 PERSPECTIVE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

```

APPLICATION NUMBER: US/08/487,487
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,201
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.962.4810
TELEFAX: 202.962.8300
INFORMATION FOR SEQ. IN NO. 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (pre-miR)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-487-007-71

Query Match 54.4%; Score 13.6; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 2; 1e-03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 TTCTTTCTATGCTGCTT 20
      |||||
      8 TGCTTTCTATGCTGCTT 27

RESULT 19
US-08-483-5548-71
Sequence 71, Application US/08483548
Patent No. 5747282
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q linked breast and ovarian cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1900
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,201
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.962.4810
TELEFAX: 202.962.8300
INFORMATION FOR SEQ. IN NO. 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-483-5548-71

Query Match 54.4%; Score 13.6; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 2; 1e-03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 TTCTTTCTATGCTGCTT 20
      |||||
      8 TGCTTTCTATGCTGCTT 27

RESULT 20
US-08-488-0118-71
Sequence 71, Application US/084880118
Patent No. 5753441
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q linked breast and ovarian cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1900
CITY: Washington
STATE: DC

```





```

Sequence 10, Application US/08791883
Patent No. 5879890
GENERAL INFORMATION:
APPLICANT: LAKEN, STEVE
APPLICANT: GRUBER, STEPHEN
APPLICANT: PERPSEN, GLOEIA
APPLICANT: KINTNER, KENNETH
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: APOPTATION ASSOCIATED WITH
TITLE OF INVENTION: FAMILIAL COLONIAL CANCER IN ASHERNATI JEWS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner & Mitcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,883
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 01107 03734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9299
TELEFAX: 202-508-9299
TELEX: 97430 BMR UT
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-791 883-10

Query Match 54.4% Score 13.6; DB 2; Length 25;
Post Local Similarity 80.0% Freq No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 TTTCTTTTATTTCTTT 20
Db 21 TTTCTTTTCTCTCTATT 2

RESULT 16
US-08-784-71
Sequence 71, Application US/0800784
Patent No. 6019401
GENERAL INFORMATION:
APPLICANT: LAKEN, STEVE
APPLICANT: GRUBER, STEPHEN
APPLICANT: PERPSEN, GLOEIA
APPLICANT: KINTNER, KENNETH
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: APOPTATION ASSOCIATED WITH
TITLE OF INVENTION: FAMILIAL COLONIAL CANCER IN ASHERNATI JEWS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner & Mitcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC

```

```

COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,843
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/791,883
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 01107 03734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 97430 BMR UT
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-023-673-10

Query Match 54.4% Score 13.6; DB 3; Length 25;
Post Local Similarity 80.0% Freq No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 TTTCTTTTATTTCTTT 20
Db 21 TTTCTTTTCTCTCTATT 2

RESULT 16
US-08-480-784-71
Sequence 71, Application US/0800784
Patent No. 5693473
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldfarb, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Yamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Sharlock-Fidens, Donna M.
APPLICANT: Tavligian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-linked Prostate and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSER: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Polyscan #1 v. Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
FILING DATE:
CLASSIFICATION: 435

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SEQ ID NO 34  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence  
US-08-864-473-34

Query Match: 55.2% Score 13.8; DB 3; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTCTTCTATGCTG 18  
|||||  
DB 18 TTTCTTCTTCTGCTG 2

RESULT 8  
US-08-864-473-36/C  
Sequence 36, Application US/08864473  
Patent No. 6027889  
GENERAL INFORMATION:  
APPLICANT: Barany, Francis  
APPLICANT: Lubin, Matthew  
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING  
TITLE OF INVENTION: COMBINED LIASER DETECTION AND POLYMERASE CHAIN REACTION  
FILE REFERENCE: 19603/441  
CURRENT APPLICATION NUMBER: US/08/864,473  
CURRENT FILING DATE: 1999-11-15  
EARLIER APPLICATION NUMBER: 60/018,532  
EARLIER FILING DATE: 1996-05-29  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence  
US-08-864-473-36

Query Match: 55.2% Score 13.8; DB 3; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTCTTCTATGCTG 18  
|||||  
DB 18 TTTCTTCTTCTGCTG 2

RESULT 9  
US-09-440-523-34/C  
Sequence 34, Application US/09440523  
Patent No. 6268148  
GENERAL INFORMATION:  
APPLICANT: Barany, Francis  
APPLICANT: Lubin, Matthew  
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING  
TITLE OF INVENTION: COMBINED LIASER DETECTION AND POLYMERASE CHAIN REACTION  
FILE REFERENCE: 19603/441  
CURRENT APPLICATION NUMBER: US/09/440,523  
CURRENT FILING DATE: 1997-11-15  
PRIOR APPLICATION NUMBER: 08/864,473  
PRIOR FILING DATE: 1997-05-28  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 34  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:

OTHER INFORMATION: Description of Artificial Sequence  
OTHER INFORMATION: Oligonucleotide Sequence  
US-09-440-523-34

Query Match: 55.2% Score 13.8; DB 4; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTCTTCTATGCTG 18  
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DB 18 TTTCTTCTTCTGCTG 2

RESULT 10  
US-09-440-523-36/C  
Sequence 36, Application US/09440523  
Patent No. 6268148  
GENERAL INFORMATION:  
APPLICANT: Barany, Francis  
APPLICANT: Lubin, Matthew  
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING  
TITLE OF INVENTION: COMBINED LIASER DETECTION AND POLYMERASE CHAIN REACTION  
FILE REFERENCE: 19603/441  
CURRENT APPLICATION NUMBER: US/09/440,523  
CURRENT FILING DATE: 1999-11-15  
PRIOR APPLICATION NUMBER: 08/864,473  
PRIOR FILING DATE: 1997-05-28  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence  
US-09-440-523-36

Query Match: 55.2% Score 13.8; DB 4; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTCTTCTATGCTG 18  
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DB 18 TTTCTTCTTCTGCTG 2

RESULT 11  
US-08-117-952-23/C  
Sequence 23, Application US/08117052  
Patent No. 5851760  
GENERAL INFORMATION:  
APPLICANT: Evans, Glen A.  
APPLICANT: Smith, Michael W.  
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE  
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES  
NAMES OF SEQUENCES: 797  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,952  
FILING DATE: 07-SEP-1993  
CLASSIFICATION: 435

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1  ZIP: 20004
2  COMPUTER READABLE FORM.
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC DOS/MS-DOS
6  SOFTWARE: Patentin Release #1.0, Version #1.25
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/09/241,149
9  FILING DATE:
10 CLASSIFICATION: 435
11 ATTORNEY/AGENT INFORMATION:
12 NAME: ABERBACH, JEFFREY I
13 RESISTANCE NUMBER: 32,490
14 REFERENCE/DOCKET NUMBER: 639-105
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (202) 383 7451
17 TELEFAX: (202) 383 7450
18 INFORMATION FOR SEQ ID NO. 8:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 39 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: DNA (genomic)
25 HYPOTHEICAL: NO
26 ANTI SENSE: NO
27 ORIGINAL SOURCE:
28 ORGANISM: Equus caballus
29 IMMEDIATE SOURCE:
30 CLONE: 1210
31 US-09-341-148-9
32
33 Query Match 56.0% Score 14 DB 1 Length 30;
34 Best Local Similarity 77.3% Pval No 1.5e+03;
35 Matches 17, Conservative 0, Mismatches 5, Gaps 0,
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981 10.2 40.8 32 4 US-09-438-331-109 Sequence 109, App
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983 10.2 40.8 33 1 US-08-314-309A-16 Sequence 16, Appli
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988 10.2 40.8 33 3 US-08-631-319A-2 Sequence 18, Appli
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## ALIGNMENTS

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RESULT 1
US-09-157-177-66/C
Sequence 66, Application US/09157177
Patent No. 6039598
GENERAL INFORMATION:
APPLICANT: Butler, John M.
APPLICANT: Li, Jia
APPLICANT: Madsen, Joseph A.
APPLICANT: Pappas, Michael B.
TITLE OF INVENTION: IMITATING BY MASS DECRYPTION WITH POLYMORPHIC DNA
FILE REFERENCE: GENE-017/GETP017P
CURRENT FILING DATE: 1998-09-18
EARLIER FILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 66
LENGTH: 24
TYPE: DNA
ORGANISM: Homo sapiens
US-09-157-177-66

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Query Match 58.41, Score 14.6, DB 3, Length 24;
Best Local Similarity 91.01, Pred. No. 9, Idents 4, Mismatches 0, Gaps 0;
Matches 17, Conservative 0, Indels 0;
DB 21 TTTTATATGTTGTTGA 1

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RESULT 2
US-09-051-079-2
Sequence 2, Application US/09051079A
Patent No. 6214949
GENERAL INFORMATION:
APPLICANT: WEINDEL, FULT
APPLICANT: SEIDEL, GRISEGH
APPLICANT: LAGGONCER, GERHARD
TITLE OF INVENTION: METHOD OF IDENTIFYING A SUBSTANCE TO BE ANALYZED
FILE REFERENCE: 101614-07096
OTHER INFORMATION: Number US/09/051-079A

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CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PCT/EP94/04358
EARLIER FILING DATE: 1996-10-08
EARLIER APPLICATION NUMBER: EP/95 17 952.7
EARLIER FILING DATE: 1996-10-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 2
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)
OTHER INFORMATION: a conserved band with PNP-TGA.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Clp has with 10.10.11e
US-09-051-079-2

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Query Match 57.61, Score 14.4, DB 4, Length 31;
Best Local Similarity 95.78, Pred. No. 1, Idents 6, Mismatches 0, Gaps 0;
Matches 18, Conservative 0, Indels 0;
DB 4 TTTTATATGTTGTTGTTG 27

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RESULT 3
US-09-560-594-89
Sequence 89, Application US/09560594
Patent No. 6245390
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ARTIFICIAL SEQUENCES OF 21NT FINGER PRINTING WITH EXPANSION
FILE REFERENCE: RPS-0144
CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 89
SEQ ID NO: 89
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially designed oligonucleotide
US-09-560-594-89

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Query Match 56.81, Score 14.2, DB 4, Length 20;
Best Local Similarity 84.21, Pred. No. 1, Idents 3, Mismatches 0, Gaps 0;
Matches 16, Conservative 0, Indels 0;
DB 3 TTTTATATGTTGTTG 21

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RESULT 4
US-08-341-148-8/C
Sequence 8, Application US/08341148
Patent No. 5610287
GENERAL INFORMATION:
APPLICANT: NIKIFOROV, THEO
APPLICANT: KNAPP, MICHAEL
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF NUCLEIC
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESS: HOWREY & SIMEN
STREET: 1209 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA

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685	10.4	41.6	24.4	US-09-144-170-16	Sequence 16, Appl	752	10.4	41.6	32.2	US-08-484-575A-1	Sequence 9, Appl
C 686	10.4	41.6	24.4	US-09-144-170-17	Sequence 17, Appl	753	10.4	41.6	32.2	US-08-484-575A-4	Sequence 9, Appl
C 687	10.4	41.6	24.4	US-09-144-170-18	Sequence 18, Appl	754	10.4	41.6	32.2	US-08-484-575A-7	Sequence 9, Appl
C 688	10.4	41.6	24.4	US-09-144-170-19	Sequence 19, Appl	755	10.4	41.6	32.2	US-08-484-575A-10	Sequence 9, Appl
C 689	10.4	41.6	24.4	US-09-144-170-20	Sequence 20, Appl	756	10.4	41.6	32.2	US-08-484-575A-13	Sequence 9, Appl
C 690	10.4	41.6	24.4	US-09-144-170-21	Sequence 21, Appl	757	10.4	41.6	32.2	US-08-484-575A-16	Sequence 9, Appl
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C 694	10.4	41.6	24.4	US-09-144-170-25	Sequence 25, Appl	761	10.4	41.6	32.2	US-08-484-575A-28	Sequence 9, Appl
C 695	10.4	41.6	24.4	US-09-144-170-26	Sequence 26, Appl	762	10.4	41.6	32.2	US-08-484-575A-31	Sequence 9, Appl
C 696	10.4	41.6	24.4	US-09-144-170-27	Sequence 27, Appl	763	10.4	41.6	32.2	US-08-484-575A-34	Sequence 9, Appl
C 697	10.4	41.6	24.4	US-09-144-170-28	Sequence 28, Appl	764	10.4	41.6	32.2	US-08-484-575A-37	Sequence 9, Appl
C 698	10.4	41.6	24.4	US-09-144-170-29	Sequence 29, Appl	765	10.4	41.6	32.2	US-08-484-575A-40	Sequence 9, Appl
C 699	10.4	41.6	24.4	US-09-144-170-30	Sequence 30, Appl	766	10.4	41.6	32.2	US-08-484-575A-43	Sequence 9, Appl
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C 701	10.4	41.6	24.4	US-09-144-170-32	Sequence 32, Appl	768	10.4	41.6	32.2	US-08-484-575A-49	Sequence 9, Appl
C 702	10.4	41.6	24.4	US-09-144-170-33	Sequence 33, Appl	769	10.4	41.6	32.2	US-08-484-575A-52	Sequence 9, Appl
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C 706	10.4	41.6	24.4	US-09-144-170-37	Sequence 37, Appl	773	10.4	41.6	32.2	US-08-484-575A-64	Sequence 9, Appl
C 707	10.4	41.6	24.4	US-09-144-170-38	Sequence 38, Appl	774	10.4	41.6	32.2	US-08-484-575A-67	Sequence 9, Appl
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C 710	10.4	41.6	24.4	US-09-144-170-41	Sequence 41, Appl	777	10.4	41.6	32.2	US-08-484-575A-76	Sequence 9, Appl
C 711	10.4	41.6	24.4	US-09-144-170-42	Sequence 42, Appl	778	10.4	41.6	32.2	US-08-484-575A-79	Sequence 9, Appl
C 712	10.4	41.6	24.4	US-09-144-170-43	Sequence 43, Appl	779	10.4	41.6	32.2	US-08-484-575A-82	Sequence 9, Appl
C 713	10.4	41.6	24.4	US-09-144-170-44	Sequence 44, Appl	780	10.4	41.6	32.2	US-08-484-575A-85	Sequence 9, Appl
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C 394	10.8	41.2	23.4	US-09-092-037-47	Sequence 17, Appl	C 464	10.6	42.4	20.4	US-09-066-104-56	Sequence 56, Appl
C 394	10.8	41.2	23.4	US-09-092-037-48	Sequence 18, Appl	C 464	10.6	42.4	20.4	US-09-066-104-57	Sequence 57, Appl
C 395	10.8	41.2	24.1	US-09-092-094-34	Sequence 5, Appl	C 464	10.6	42.4	20.4	US-09-066-104-58	Sequence 58, Appl
C 396	10.8	41.2	24.1	US-09-092-126-14	Sequence 14, Appl	C 464	10.6	42.4	20.4	US-09-066-104-59	Sequence 59, Appl
C 397	10.8	41.2	24.2	US-09-092-088-14	Sequence 14, Appl	C 470	10.6	42.4	21.1	US-09-092-073-116	Sequence 116, Appl
C 398	10.8	41.2	24.3	US-09-092-113-44	Sequence 44, Appl	C 471	10.6	42.4	21.1	US-09-092-073-117	Sequence 117, Appl
C 399	10.8	41.2	24.4	US-09-092-182-9	Sequence 9, Appl	C 472	10.6	42.4	21.1	US-09-092-073-118	Sequence 118, Appl
C 400	10.8	41.2	25.1	US-09-092-074-13	Sequence 13, Appl	C 473	10.6	42.4	21.1	US-09-092-073-119	Sequence 119, Appl
C 401	10.8	41.2	25.1	US-09-092-074-14	Sequence 14, Appl	C 474	10.6	42.4	21.1	US-09-092-073-120	Sequence 120, Appl
C 402	10.8	41.2	25.2	US-09-092-074-15	Sequence 15, Appl	C 475	10.6	42.4	21.1	US-09-092-073-121	Sequence 121, Appl
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C 405	10.8	41.2	25.5	US-09-092-074-18	Sequence 18, Appl	C 478	10.6	42.4	21.1	US-09-092-073-124	Sequence 124, Appl
C 406	10.8	41.2	25.6	US-09-092-074-19	Sequence 19, Appl	C 479	10.6	42.4	21.1	US-09-092-073-125	Sequence 125, Appl
C 407	10.8	41.2	25.7	US-09-092-074-20	Sequence 20, Appl	C 480	10.6	42.4	21.1	US-09-092-073-126	Sequence 126, Appl
C 408	10.8	41.2	25.8	US-09-092-074-21	Sequence 21, Appl	C 481	10.6	42.4	21.1	US-09-092-073-127	Sequence 127, Appl
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C 411	10.8	41.2	26.1	US-09-092-074-24	Sequence 24, Appl	C 484	10.6	42.4	21.1	US-09-092-073-130	Sequence 130, Appl
C 412	10.8	41.2	26.2	US-09-092-074-25	Sequence 25, Appl	C 485	10.6	42.4	21.1	US-09-092-073-131	Sequence 131, Appl
C 413	10.8	41.2	26.3	US-09-092-074-26	Sequence 26, Appl	C 486	10.6	42.4	21.1	US-09-092-073-132	Sequence 132, Appl
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C 415	10.8	41.2	26.5	US-09-092-074-28	Sequence 28, Appl	C 488	10.6	42.4	21.1	US-09-092-073-134	Sequence 134, Appl
C 416	10.8	41.2	26.6	US-09-092-074-29	Sequence 29, Appl	C 489	10.6	42.4	21.1	US-09-092-073-135	Sequence 135, Appl
C 417	10.8	41.2	26.7	US-09-092-074-30	Sequence 30, Appl	C 490	10.6	42.4	21.1	US-09-092-073-136	Sequence 136, Appl
C 418	10.8	41.2	26.8	US-09-092-074-31	Sequence 31, Appl	C 491	10.6	42.4	21.1	US-09-092-073-137	Sequence 137, Appl
C 419	10.8	41.2	26.9	US-09-092-074-32	Sequence 32, Appl	C 492	10.6	42.4	21.1	US-09-092-073-138	Sequence 138, Appl
C 420	10.8	41.2	27.0	US-09-092-074-33	Sequence 33, Appl	C 493	10.6	42.4	21.1	US-09-092-073-139	Sequence 139, Appl
C 421	10.8	41.2	27.1	US-09-092-074-34	Sequence 34, Appl	C 494	10.6	42.4	21.1	US-09-092-073-140	Sequence 140, Appl
C 422	10.8	41.2	27.2	US-09-							





Wed Jul 23 09:24:58 2003

us-09-890-363-6.max.mli

GenCore version 5.1.6  
(c) 1993 - 2003 Compugen Ltd.

GenCore - nucleic search, using sw model  
July 21, 2003, 11:41:02 : Search time 19.1617 seconds  
(without alignments)  
400.117 Million cell w/first/sec

US-09-890-363-6

Title: 25  
Perfect score: 1  
Sequence: 1  
Gapop 10.0  
Gapext 1.0

Scoring table: IDENTITY NUC  
Gapop 10.0  
Gapext 1.0

441362 seqs, 15338381 residues

499442

Minimum Match 100%

Maximum Match 100%

Listing first 1000 summaries

Issued: Patents HA.\*  
1: /cgn2\_6/prodata/1/ina/64.COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/64.COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/64.COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/64.COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/64.COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/64.COMB.seq.\*

pred. H: is the number of results predicted by chance to have a  
score greater than or equal to the total score distribution.  
and is derived by analysis of

SUMMARIES

Description

Result	Score	Match length	DB	ID
1	58.4	24	US-09-051-579-2	Sequence 66, Appl
2	14.6	31	US-09-051-579-2	Sequence 2, Appl
3	14.6	26	US-09-051-579-2	Sequence 4, Appl
4	14.6	26	US-09-051-579-2	Sequence 8, Appl
5	14.6	26	US-09-051-579-2	Sequence 16, Appl
6	14.6	26	US-09-051-579-2	Sequence 34, Appl
7	14.6	26	US-09-051-579-2	Sequence 36, Appl
8	14.6	26	US-09-051-579-2	Sequence 38, Appl
9	14.6	26	US-09-051-579-2	Sequence 40, Appl
10	14.6	26	US-09-051-579-2	Sequence 42, Appl
11	14.6	26	US-09-051-579-2	Sequence 44, Appl
12	14.6	26	US-09-051-579-2	Sequence 46, Appl
13	14.6	26	US-09-051-579-2	Sequence 48, Appl
14	14.6	26	US-09-051-579-2	Sequence 50, Appl
15	14.6	26	US-09-051-579-2	Sequence 52, Appl
16	14.6	26	US-09-051-579-2	Sequence 54, Appl
17	14.6	26	US-09-051-579-2	Sequence 56, Appl
18	14.6	26	US-09-051-579-2	Sequence 58, Appl
19	14.6	26	US-09-051-579-2	Sequence 60, Appl
20	14.6	26	US-09-051-579-2	Sequence 62, Appl
21	14.6	26	US-09-051-579-2	Sequence 64, Appl
22	14.6	26	US-09-051-579-2	Sequence 66, Appl
23	14.6	26	US-09-051-579-2	Sequence 68, Appl
24	14.6	26	US-09-051-579-2	Sequence 70, Appl
25	14.6	26	US-09-051-579-2	Sequence 72, Appl
26	14.6	26	US-09-051-579-2	Sequence 74, Appl
27	14.6	26	US-09-051-579-2	Sequence 76, Appl

28	13.4	53.6	US-09-678-437-101	Sequence 101, App
29	13.2	52.8	US-09-072-384-12	Sequence 12, Appl
30	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
31	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
32	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
33	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
34	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
35	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
36	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
37	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
38	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
39	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
40	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
41	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
42	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
43	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
44	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
45	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
46	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
47	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
48	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
49	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
50	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
51	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
52	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
53	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
54	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
55	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
56	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
57	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
58	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
59	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
60	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
61	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
62	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
63	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
64	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
65	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
66	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
67	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
68	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
69	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
70	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
71	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
72	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
73	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
74	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
75	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
76	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
77	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
78	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
79	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
80	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
81	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
82	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
83	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
84	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
85	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
86	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
87	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
88	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
89	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
90	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
91	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
92	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
93	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
94	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
95	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
96	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
97	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
98	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
99	13.2	52.8	US-09-072-384-12	Sequence 30, Appl
100	13.2	52.8	US-09-072-384-12	Sequence 30, Appl



CC subsequent cloning of the gene responsible for the trait, the products  
 CC of the invention may also be used for treatment or prevention of the  
 CC specified diseases  
 XX  
 SC Sequence 31 BP; 5 A; 4 C; 10 G; 11 T; 1 other;  
 Query Match 54.4%, Score 13.6, DB 20, Length 31;  
 Best local similarity 72.0%, Prod No 1 72.04,  
 Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TTTCTTTCTGATGCTGCTG 22  
 ||||| ||||| |||||  
 DB 1 TTTCTGCTGATGCTGCTG 22  
 RESULT 39  
 AAV72843  
 ID AAV72843 standard; DNA; 33 BP.  
 XX  
 AC AAV72843;  
 XX  
 DT 19 FEB-1999 (first entry)  
 XX  
 DE Human interferon gamma 1 probe.  
 XX  
 KW Human; interferon 4; IL 4; PCR primer; filter optic biosensor;  
 KW detection; filter; hybridization; optical fiber; bio  
 XX  
 OS Synthetic.  
 XX  
 SN Homo sapiens.  
 XX  
 EX WC9850782-A2.  
 XX  
 PD 12-NOV 1998.  
 XX  
 PF 05-MAY-1998; 98MO-US09163.  
 XX  
 PR 05-MAY-1997; 97PS-0957203  
 XX  
 PA (TQFT) TQFTS COLLEGE.  
 XX  
 PI Ferguson JR, Healey BG, Walt DP;  
 XX  
 DP WPI; 1998-610511/51.  
 XX  
 PT Filter optic biosensor for selectively detecting oligonucleotide  
 XX specific has single stranded oligonucleotide in situ hybridization  
 XX zone defined as topcoat on end face surface of filter film.  
 XX  
 RS Disclosure; Page 45; 89pp; English.  
 XX  
 CC An optical biosensor has been developed which includes a plan optical  
 CC fibre strand (10) which presents two strand end faces (16,18) as  
 CC discrete fibre surfaces for illumination and emergence of light energy.  
 CC Also described in the present invention are (i) an oligonucleotide  
 CC in situ hybridization zone configuration the specific of single stranded  
 CC oligonucleotide is disposed as a deposit upon the end face and serves as  
 CC a diffuser, single-specific, fixed probe suitable for selective in situ  
 CC hybridization combined with a multi-reflective layer (12) and (ii) a  
 CC larger specific (20) any complementary oligonucleotide larger probe  
 CC hybridized in situ ultimately bears a joined layer (12) (13) (14)  
 CC comprising a light energy absorbing dye of known optical characteristics.  
 CC The resulting specific specific, in situ hybridized oligonucleotide  
 CC reaction product formed in the hybridization zone is specifically  
 CC detected with the optical fibre device by the joined identifying  
 CC label concomitantly disposed at the strand end face surface. The  
 CC biosensor overcomes and eliminates most, if not all, of the major  
 CC limitations and drawbacks hindrances such as the problems of assay  
 CC sensitivity, lengthy analysis times and the quantum of background signal  
 CC noise. The present sequence represents a probe for human interferon  
 CC gamma 1 from the present invention.  
 XX  
 SC Sequence 33 BP; 1 A; 4 C; 6 G; 22 T; 0 other;

QY 1 TTTCTTTCTGATGCTGCTG 22  
 ||||| ||||| |||||  
 DB 1 TTTCTGCTGATGCTGCTG 22  
 RESULT 40  
 ABUS6697  
 ID ABUS6697 standard; DNA; 33 BP.  
 XX  
 AC ABUS6697;  
 XX  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE PCR primer #4 for polyadenylation binding protein 20.13 cDNA.  
 XX  
 KW Human; polyadenylation binding protein 20.13;  
 KW entry; development; disorder; growth developmental; disturbance; disease;  
 KW gene therapy; PCR; primer; seq.  
 XX  
 OS Homo sapiens.  
 XX  
 EX WC020000072-A1.  
 XX  
 PD 04 APR 2002.  
 XX  
 PF 20-AUG-2001; 2001MO-CNO1259.  
 XX  
 PR 23 AUG 2000; 2000CN-0119744.  
 XX  
 PA (SHAN) SHANGHAI BIORINCOR GENETIC INC.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DP WPI; 2002-281207/22.  
 XX  
 PT New human polyadenylation binding protein 20.13 for diagnosis and  
 PT treating embryonic development disorders and growth developmental  
 PT disturbance diseases.  
 XX  
 RS Example 5; Page 18; 36pp; Chinese.  
 XX  
 CC 15 filaments are used as well as to amplify alpha globulin human  
 CC polyadenylation binding protein 20.13. The filaments and  
 CC polynucleotide are used in diagnosis and treatment of embryo  
 CC development disorders and growth developmental disturbance diseases.  
 CC The polynucleotide may also be used for gene therapy.  
 XX  
 SC Sequence 33 BP; 7 A; 8 C; 8 G; 10 T; 0 other;  
 Query Match 54.4%, Score 13.6, DB 24, Length 33;  
 Best local similarity 70.0%, Prod No 1 70.04,  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TTTCTTTCTGATGCTGCTG 22  
 ||||| ||||| |||||  
 DB 7 TTTCTATTTCTGCTGCTG 22  
 Search completed: 0.07 sec; 1998-09-29  
 Job time: 35.44 sec

XX  
 PN W0200065088 A2.  
 XX  
 PD 02 NOV 2000  
 XX  
 PF 20 APR 2000; 2000W0-EPO3636.  
 XX  
 PR 26 APR 1999; 99EP-0303215.  
 XX  
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.  
 XX  
 PI Utendahl P, Wong K;  
 DR WPI; 2000-679677/66.  
 XX  
 PT Identifying extendible primers for use in identification, or  
 PT classification of a nucleic acid of an organism, allele or gene such as  
 PT class 1/2 HLA sequences identifying all 16 HLA sequences  
 PT of specific length  
 XX  
 PS Claim 14; Page 46; 66pp; English.  
 XX  
 CC The present invention provides a method for identifying a set of  
 CC extendible primers which can be used in the identification, typing and  
 CC classification of genes. This can then be used to predict protein and  
 CC sequence and structure, in organ donation to match the organ with the  
 CC receiver, and to identify bacteria in a sample. The method can be used to  
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
 CC particular.  
 XX  
 SQ Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 other;  
 Query Match 54.4%; Score 12.6; 15.7; Length 25;  
 Best local similarity 80.0%; Pred. No. 1.9e+04;  
 Matches 16; Conservative 0; Mismatched 4; In gaps 0; Gaps 0;  
 1 TTTCTTTCTATGCTGCTT 20  
 3 TTTTCTTTCTGCTGCTT 22

RESULT 37  
 AAC96153  
 ID AAC96153 standard; DNA; 25 BP.  
 XX  
 AC AAC96153;  
 XX  
 DT 26 FEB-2001 (first entry)  
 XX  
 DE 16s rRNA gene PCR primer #120.  
 XX  
 EM DNA sequence analysis, sequencing; protein sequence; protein structure;  
 EM gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
 FM human leukocyte antigen PCR primer; ss.  
 XX  
 OS Homo sapiens  
 XX  
 PN W0200065088 A2.  
 PD 02 NOV 2000;  
 XX  
 PF 20 APR 2000; 2000W0-EPO3636.  
 XX  
 PR 26 APR 1999; 99EP-0303215.  
 XX  
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.  
 XX  
 PI Utendahl P, Wong K;  
 DR WPI; 2000-679677/66.  
 XX  
 PT Identifying extendible primers for use in identification, or  
 PT classification of a nucleic acid of an organism, allele or gene such as  
 PT class 1/2 HLA sequences identifying all 16 HLA sequences  
 PT of specific length

PT class 1/2 HLA sequences identifying all 16 HLA sequences  
 PT of specific length  
 XX  
 PS Claim 14; Page 46; 66pp; English.  
 XX  
 CC The present invention provides a method for identifying a set of  
 CC extendible primers which can be used in the identification, typing and  
 CC classification of genes. This can then be used to predict protein and  
 CC sequence and structure, in organ donation to match the organ with the  
 CC receiver, and to identify bacteria in a sample. The method can be used to  
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
 CC particular.  
 XX  
 SQ Sequence 25 BP; 2 A; 1 C; 3 G; 19 T; 0 other;  
 Query Match 54.4%; Score 12.6; 15.7; Length 25;  
 Best local similarity 80.0%; Pred. No. 1.9e+04;  
 Matches 16; Conservative 0; Mismatched 4; In gaps 0; Gaps 0;  
 1 TTTCTTTCTATGCTGCTT 20  
 6 TTTTCTTTCTGCTGCTT 25

RESULT 38  
 AAX38575  
 ID AAX38575 standard; DNA; 31 BP.  
 XX  
 AC AAX38575;  
 XX  
 DT 15-JUN-1999 (first entry)  
 XX  
 LE Human gelatinase DNA polymerase alpha subunit cDNA  
 XX  
 KW Polymorphic sites, human, forensic, paternity testing, fingerprinting,  
 KW diagnosis, disease susceptibility, autoimmune disease, infectious disease,  
 KW inflammatory disease, gene expression, human, forensic, fingerprinting,  
 KW physical characteristics, heredity, breeding programs, linkage, locus,  
 KW gene mapping; treatment; prevention; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09014228-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-US19325.  
 XX  
 PE 14-NOV-1997; 97US-0056172.  
 XX  
 FR 17-SEP-1997; 97US-0059304.  
 XX  
 PA (AFFIX) AFFIMETRIX INC.  
 XX  
 PI Bernd A, Chee M, Fan J, Lipschutz RJ;  
 XX  
 DP WPI; 1999-029497/19.  
 XX  
 FT Nucleic acid encoding specific human polymorphisms  
 XX  
 PS Claim 1; Page 9; 56pp; English.  
 XX  
 CC This invention describes nucleic acid segments represented in  
 CC AAX18554-X19498 which are isolated from any of about 750 human genomic  
 CC regions given in the specification that include a polymorphic site, or  
 CC their complements. Analysis of the polymorphisms is useful (1) to  
 CC identify individuals for forensic studies and paternity testing, (2) to  
 CC correlate the polymorphisms with phenotypic traits, e.g. the diseases  
 CC (1) it associates with, (3) with range of diseases including autoimmune,  
 CC inflammatory and nervous system disorders, cancer, infectious diseases,  
 CC longevity, physical characteristics, response to drug or therapy, also  
 CC in animals and plants to identify individuals for breeding programs, (4)  
 CC to identify physical linkage between recessive acid segments and a  
 CC specific genetic trait, and (5) to be used with a trait for gene mapping and for





OS Synthetic.  
 XX  
 PN WO9429486 A.  
 XX  
 PD 22-DEC-1994.  
 XX  
 PF 15-JUN-1994; 94WO-US06810.  
 XX  
 PR 15-JUN-1994; 93US-6078471.  
 PR 07-SEP-1993; 93US-0117952.  
 XX  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 PI Evans GA, Smith MW;  
 XX  
 DR WPI; 1996-016508/05.  
 XX  
 PT Sequencing complex genomes, present as fragments in a cosmid  
 PT library, by sequencing oligonucleotide subclones of each clone  
 PT then correlating with spatial relationship of cosmid, esp. for  
 PT mammalian chromosomes.  
 XX  
 PS Example 4; Page 62; 128pp; English.  
 XX  
 CC Sequences were determined from the ends of chromosome 11-specific  
 CC cosmids by automated sequencing without intermediate subcloning.  
 CC  
 CC A sample of 371 DNA sequence fragments were determined and of  
 CC these, 277 were suitable for STS primer identification by computer  
 CC analysis (using the "primer" program available from E. Landier, MIT).  
 CC The STSs and cosmids were mapped by in situ hybridisation, somatic  
 CC cell hybrid analysis or both. Using this method, 370 STSs specific  
 CC for human chromosome 11 were generated and most of them were  
 CC regionally mapped. This procedure illustrates a novel method for  
 CC sequencing complex genomes, designated "sequence sampled mapping".  
 CC The sequence sampled mapping method is useful for the completion of  
 CC high density sequence-based maps, and ultimately, for the complete  
 CC sequencing of genomic DNA directly from cosmid clones.  
 CC See AAO82001-082706 for STS primers.  
 CC  
 CC Sequence 22 BP; 14 A, 6 C, 1 G, 1 T, 0 other;  
 CC  
 CC Query Match 54.4%; Score 13.6; DB 16; Length 22;  
 CC Best Local Similarity 86.0%; Field No. 14;  
 CC Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 CC  
 CC 5 TTTTCTATGCTGCTGCTG 24  
 CC |||||  
 CC 22 TTTCTTTGATGATGCTG 3  
 CC  
 CC RESULT 12  
 CC AAT15885/c  
 CC ID AAT15885 standard; DNA; 24 BP.  
 CC  
 CC AAT15885;  
 CC  
 CC 14 MAY-1996 (first entry)  
 CC  
 CC CD44 gene PCR primer Sp1  
 CC  
 CC CD44; exon 3, tumour, nonplasm, metastasis, bladder cancer,  
 CC prostate, diathesis, polymerase chain reaction, PCR, primer; ss.  
 CC  
 CC Symbolic.  
 CC  
 CC WO9603527 A2.  
 CC  
 CC 08 FEB-1996.  
 CC  
 CC 21-JUN-1995; 95WO-G801741.  
 CC  
 CC 16 MAY-1995; 95SR-066386.  
 CC  
 CC 21-JUN-1994; 94SP-0014704

PR 17 OCT-1994; 94GB-0020878.  
 XX  
 XX (ISIS-) ISIS INNOVATION LTD.  
 XX  
 XX Matsumura Y, Tarin D;  
 XX  
 DR WPI; 1996-11/068/12.  
 XX  
 XX Probes for mammalian CD44 gene, from 3 and exon 9a sequences  
 XX isolated from tumour cells, used for the diagnosis of neoplasia or  
 XX metastasis  
 XX  
 PS Disclosure, Page 16; 27pp; English.  
 XX  
 CC Primers Sp1 (AAT15885) and Sp2 (AAT15886) were used to amplify cDNA  
 CC derived from bladder carcinoma F112 cells, normal bladder tissue,  
 CC bladder cancer tissue, normal urinary cell sediment, and urine  
 CC cell sediment. The products were used in Southern hybridizations  
 CC using probes for exon 3, 141 bp 3' (AAT15884) and exon 9a (AAT15885).  
 CC exon 7 and exon 15 of the CD44 gene.  
 CC  
 CC Sequence 24 BP; 9 A, 7 C, 6 G, 2 T, 0 other;  
 CC  
 CC Query Match 54.4%; Score 13.6; DB 17; Length 24;  
 CC Best Local Similarity 86.0%; Field No. 14;  
 CC Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 CC  
 CC 24 TTTTCTATGCTGCTGCTG 25  
 CC |||||  
 CC 24 TTTTCTATGCTGCTGCTG 5  
 CC  
 CC RESULT 13  
 CC AAV43856/c  
 CC ID AAV43856 standard; DNA; 24 BP.  
 CC  
 CC AAV43856;  
 CC  
 CC 26-OCT-1998 (first entry)  
 CC  
 CC APC wild-type gene specific oligonucleotide.  
 CC  
 CC APC; human colorectal cancer; PCR; miscense mutation; Adkinman; Jew;  
 CC mutation analysis; hybridisation; ss.  
 CC  
 CC Synthetic.  
 CC  
 CC Homo sapiens.  
 CC  
 CC WO9833940-A1.  
 CC  
 CC 06-AUG-1998.  
 CC  
 CC 21-JAN-1998; 98WO-US00961.  
 CC  
 CC 31-JAN-1997; 97US-0791883.  
 CC  
 CC (UNCO ) UNIV JOHNS HOPKINS.  
 CC  
 CC Gruber S, Kinzler K, Laken S, Petersen G, Vogelstein B;  
 CC  
 CC WPI; 1998-437490/37.  
 CC  
 CC Detection of mutation in APC gene, comprising T to A transversion  
 CC at nucleotide 1929, useful for predicting predisposition to  
 CC colorectal cancer  
 CC  
 PS Example 3; Page 11; 23pp; English.  
 XX  
 CC This oligonucleotide is specific for the wild-type APC gene sequence and  
 CC is used in the mutation analyses of the APC gene. This is used to  
 CC identify the method of the invention of detecting a mutation in APC  
 CC gene. The method uses an allele-specific probe and a probe which  
 CC comprises a nucleic acid sequence of a region of a human APC gene

CY 3 TTTTCTATGTCCTGT 19  
 ||||| |||||  
 DB 22 TTTTATATGTCCTGT 6  
  
 RESULT 29  
 AA130260/C  
 ID AA130260 standard; DNA; 31 BP.  
 XX  
 AC AA130260;  
 XX  
 DE 18-OCT-2001 (first entry)  
 XX  
 DE Human single nucleotide polymorphism (SNP) data.  
 XX  
 DE Human, race/ethnicity, genotype, disease, forensic, paternity testing,  
 XX single nucleotide polymorphism, SNP, etc.  
 XX  
 CS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Variation /replace(16,C)  
 FT /\*\*tag= a  
 FT /standard\_name "single nucleotide polymorphism"  
 XX  
 PA W0200166800-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 07-MAR-2001; 2001WU-US07268.  
 XX  
 PR 07-MAR-2001; 2000WU-0197810  
 PR 22-MAY-2000; 2000WU-0197810  
 XX  
 PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Cargill M. Ireland et al. (unpubl)  
 XX  
 DR WPI; 2001-522952/57.  
 XX  
 PT Nucleic acid sequences from the human genome which include single nucleotide polymorphisms.  
 PT sites used in methods for predicting the presence/absence of  
 PT severity of a particular form of a disease or other condition  
 PT associated with a particular genotype  
 XX  
 PS Claim 1; Page 75; 145pp; English.  
 XX  
 CC The invention relates to the identification of nucleic acid sequences  
 CC (AA129512) from the human genome which include single nucleotide polymorphisms  
 CC which can predispose individuals to disease. Various genes from a number  
 CC of individuals were sequenced and single nucleotide polymorphisms  
 CC (SNPs) in these genes were identified. The method is useful for predicting the  
 CC presence/absence of a particular form of a disease or other condition  
 CC (diabetes) associated with a particular genotype. The method also  
 CC containing the polymorphic sites may be useful in forensic and paternity  
 CC testing.  
 XX  
 SQ Sequence 31 BP; 15 A; 8 C; 3 G; 5 T; 0 other;  
  
 Query Map 1 55 31. Score 13.5. E= -4. Length 25.  
 Best Local Similarity 72.08. E= -4.1. Start Nov. 1997.  
 Matches 15. Conserved 0. Mismatch 0. Indels 0. Gap 0.  
  
 CY 1 TTTCTTTTATGTCCTGTGTA 25  
 ||||| ||||| |||||  
 DB 27 TTTCTTTTATGTCCTGTGTA 3  
  
 RESULT 30  
 AAD12815  
 ID AAD12815 standard; DNA; 72 BP  
 XX

AC AAD12815;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Solanum tuberosum gsf1 promoter (539 to +48) reverse PCR primer.  
 XX  
 DE Hyperfective response elicitor, transgene, transgenic plant, infection,  
 XX gene therapy, crop loss, antifungal, fungicide, PCR primer, etc.  
 XX  
 OS Solanum tuberosum.  
 XX  
 PN W0200155347-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001WU-US02579.  
 XX  
 PR 26-JAN-2001; 2000WU-0178565.  
 XX  
 PA (COPR) COPRHL RES FOUND INC.  
 XX  
 FH Best ST; Bauer DM;  
 FT WPI; 2001-499791/53.  
 XX  
 PS New chimeric gene, useful for controlling plant-pathogenic fungi and  
 PT producing composite resistant transgenic plants, comprising first DNA  
 FT encoding hyperinfective response elicitor, promoter and regulatory  
 PT region.  
 XX  
 PS Example 1; Page 33; 72pp; English.  
 XX  
 CC The invention relates to a chimeric gene that includes a first DNA  
 CC molecule encoding a hyperinfective response elicitor protein or  
 CC polypeptide, operably linked to the first DNA molecule  
 CC encoding a transcription of the first DNA molecule in response to  
 CC activation of the first DNA molecule and a regulatory region  
 CC operably linked to the first DNA molecule. The method also includes  
 CC a transgenic plant resistant to disease resulting from composite  
 CC infection, the transgenic plant including the chimeric gene, wherein  
 CC the promoter induces transcription of the first DNA molecule in  
 CC response to infection of the plant by a pathogen. The chimeric gene  
 CC is used in gene therapy. The chimeric gene is useful as an effective  
 CC and safe means of controlling plant pathogenic fungi, particularly  
 CC fungi which are responsible for crop loss and is also useful  
 CC for producing transgenic plants of the invention. The second sequence  
 CC is a PCR primer used to amplify Solanum tuberosum gsf1 promoter region  
 CC (539 to +48).  
 XX  
 CC Solanum tuberosum (4 A, 5 C, 3 G, 15 T; 0 other);  
 XX  
 CY Query Map 1 55 31. Score 13.5. E= -4. Length 25.  
 Best Local Similarity 88.03. E= -4.1. Start Nov. 1994.  
 Matches 15. Conserved 0. Mismatch 0. Indels 0. Gap 0.  
  
 DB 8 TTTCTATGTCCTGTGTCGT 24  
  
 RESULT 31  
 AAG20203/C  
 ID AAG20203 standard; DNA; 42 BP.  
 XX  
 AC AAG20203;  
 XX  
 DE 30-APR-1994 (first entry)  
 XX  
 DE Chromosome 11 (human distal) STS primer c11g-564-b.  
 XX  
 DE Sequence sampled (mapped); genomic analysis; composite gene map;  
 XX genetic library, human genome project; 1993-1994; gene mapping, etc.  
 XX



XX 04 FEB-1997.  
PC  
XX 97WO-US090012  
XX 27-MAY-1997;  
PF  
XX 96US-0018532.  
PR 29-MAY-1996,  
XX  
XX (COOR ) CORNELL RES FORMD INT  
PA  
XX Barany F, Belgrader P, Lubin M;  
PI  
XX WFI, 1998 030669/03  
DK  
XX Multiplex detection of nucleic acid sequence differences - using  
PT ligase detection reaction coupled to PCR, useful for determining  
PT gene dosage, for detecting genetic disorders, etc  
XX  
XX Example 8; Page 84; 158pp; English.  
PS

XX The present sequence was used in the development of three novel  
CC methods for the detection nucleic acid sequence differences, i.e.  
CC mutations, base changes, insertions, deletions or translocations. The  
CC first uses the ligase detection reaction (LDR) method to pop. The  
CC second a 1st PCR amplified to a 2nd PCR amplified to a 3rd and the 3rd a  
CC 1st PCR amplified to a 2nd PCR  
XX  
XX Sequence 21 PP, 12 A, 4 C, 6 G, 0 T, 0 other:  
SV

Query Match: 58 2%, Score 12 9; DP 19; Length 21;  
Best Uniquely Aligned Region: 100% Identical  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0

OY 2 TTCTTTTATGCTG 18  
|||||||  
Db 18 TTCTTTCTTGCTG 2

RESULT 25  
AACB960  
ID AAC96366 standard; DNA; 25 BP.  
XX  
XX AAC96366,  
AC  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DPB1 Gene POP primer #98.  
XX  
XX HLA-DPB1-01 analysis: sequencing; protein sequence; protein structure;  
XX gene typing; organ donation; bacterial identification; 16S rRNA, HMA;  
KM human leukocyte antigen; POP primer; ss.  
XX  
OS Homo sapiens.  
XX  
XX W000065968-A01  
PI  
PD 02 NOV-2000  
XX  
XX 26 APR-1997, 9609W0-EPO1636.  
PF  
XX 26-APR-1999; 99EP-0303215.  
PR  
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
XX Ulfendahl P, Wong K;  
PI  
XX WPI, 2000 670677/66.  
DR  
XX  
XX Identifying extensible primers for use in identification, or  
PT classifying, of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences  
PT of specified length -  
XX  
XX Claim 14; Page 50; 66pp; English.

CC The present invention provides a method for identifying a set of  
 CC extendible primers which can be used in the identification, typing and  
 CC classification of genes. This can often be used to predict protein  
 CC sequence and structure, in organ donation research the organ with the  
 CC sequence, and identify bacteria in a sample. The method can be used to  
 CC type the human leukocyte antigen genes (HLA) and the RNA genes  
 CC particular.  
 CC  
 CC Sequence 25 BP, 3 A, 4 C, 1 G, 15 T, 0 other;  
 CC  
 CC Query March 45.2%; Score 13.8; DB 21; Length 25;  
 CC Best Local Similarity 72.0%; Pct. No. 1.6e+04; Indels 0; Gaps  
 CC Matches 19; Conservative 0; Mismatches 7;  
 CC  
 CC 1 TTCTCTTCAATGCTGTTTCTGTA 25  
 CC ||||| ||||| ||||| ||||| |||||  
 CC 1 TTTTCTTTTCTCTCTGTAAGAA 25  
 CC ||||| ||||| ||||| ||||| |||||

```

RESULT 26
AB064555
ID      AB064555 standard; DNA; 25 BP.
XX
XX      AP064555;
XX
XX      1. AB064555 (first entry)
XX
XX      Human KCTD13 protein (AB064555) probe # 1268.
XX
XX      Protein: KCTD13; PT.M: Kidney tumor overexpressed membrane; cytosolic;
XX      Gene: KCTD13; Synonyms: KCTD13, KCTD13, KCTD13, KCTD13, KCTD13, KCTD13,
XX      KCTD13; Tissue: Kidney, Liver, Testis, Ovary, Uterus, Pancreas, Bone,
XX      Kidney; Colon; Skeletal muscle; Testis; Uterus; Pancreas; Bone;
XX
XX      Homo sapiens
XX
XX      W0200224750 AC.
XX
XX      28 MAR-2002
XX
XX      1-SHF 2001, 2001WO-US296566.
XX
XX      21-SEP-2002, 2000US-234687P.
XX      27-SEP-2002, 2000US-234659P.
XX      04-OCT-2002, 2000GB-0024263.
XX      30-JAN-2001, 2001WO-US00662.
XX      30-JAN-2001, 2001WO-US00662.
XX      30-JAN-2001, 2001WO-US00663.
XX      30-JAN-2001, 2001WO-US00664.
XX      30-JAN-2001, 2001WO-US00665.
XX      30-JAN-2001, 2001WO-US00666.
XX      30-JAN-2001, 2001WO-US00667.
XX      30-JAN-2001, 2001WO-US00668.
XX      30-JAN-2001, 2001WO-US00669.
XX      30-JAN-2001, 2001WO-US00670.
XX      27-MAY-2001, 2001US-0864761.
XX      28-AUG-2001, 2001US-215676P.
XX
XX      (AB06-) AECOMICA INC.
XX
XX      Zhang J;
XX
XX      WPI, 2002-479509/51.
XX
XX      New human kidney tumor overexpressed membrane (KCTD13) protein and
XX      PT nucleic acids encoding the protein, useful for treating subjects having
XX      PT defects in KCTD13 which can manifest as cancer of the kidney, or as a
XX      PT disorder of the liver or bone.
XX
XX      Example 2, Page 122; 419pp; English.
XX
XX      The invention relates to a novel isolated nucleic acid encoding human
XX      KCTD13 kidney tumor overexpressed membrane protein. The protein of the
XX

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XX S2 Sequence: 31 BP; 2 A; 9 C; 11 T; 0 other;  
 Query Match: 59.4%, Score 14.6, E-22, Length 31,  
 Best Local Similarity: 81.0%; Pred. No. 7.6e+03;  
 Matches: 17; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;  
 QY 4 TTTTCTTATATGCTGTTGCTG 24  
 |||||  
 Db 1 CTGTCATATGCTGTTGCTG 21  
 RESULT 13  
 AAC96594  
 ID AAC96594 standard, DNA, 25 BP.  
 AC AAC96594;  
 DT 26 FEB 2001 (first entry)  
 XX  
 DE HLA DBR345 gene PCR primer #65.  
 XX  
 KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
 KW gene; HLA; HLA identification; HLA identification; 168 bp; HLA, HLA,  
 KW human leukocyte antigen; PCR primer; ss.  
 XX  
 OS Homo sapiens  
 XX  
 PN M020065086 AL;  
 XX  
 P2 02-NOV-2000;  
 PF 20-APR-2000; 2000MO-EP03636.  
 XX  
 PP 26-APR-1999; 99EP 0303215.  
 XX  
 PA (AMSH) AMPHSHAW PHARMACIA BIOTECH AB  
 XX  
 PI Utendahl P, Wong K;  
 XX  
 DP WPI; 2000-6/9611/66;  
 XX  
 FT Identifying exons: filters for use in identification, or  
 FT classification of a nucleic acid of an organism; allele or gene such as  
 FT class 17; HLA. Willows identifying all possible nucleotide sequences  
 FT of specific length.  
 XX  
 PS Claim 14; Page 54; 66pp; English.  
 XX  
 CC The present invention provides a method for identifying a set of  
 CC exon/intron filters which can be used in the identification, typing and  
 CC classification of genes. This can then be used to predict protein  
 CC sequence and structure, in organ function to match the organ with the  
 CC receptor, and to identify bacteria in a sample. The method can be used to  
 CC type the human leukocyte antigen genes (HLA) and 168 bp; HLA genes in  
 CC particular.  
 XX  
 SQ Sequence 25 BP; 2 A; 2 C; 16 T; 0 other;  
 Query Match: 57.6%, Score 14.4, E-21, Length 25,  
 Best Local Similarity: 75.0%; Pred. No. 8.9e+03;  
 Matches: 19; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;  
 QY 1 TTTTCTTATATGCTGTTGCTG 24  
 |||||  
 Db 2 TTTTCTTATATGCTGTTGCTG 25  
 RESULT 14  
 AAV45573  
 ID AAV45573 standard, DNA, 31 BP.  
 AC AAV45573;  
 DT 05-SEP-2001 (first entry)

XX  
 LT 15-FEB-1999 (first entry)  
 XX  
 EE Human IB1 gene intron 9 exon 10 boundary.  
 XX  
 KW IB1: islet-brain 1; transcription factor; human; diabetes;  
 KW dementia; parkinson's disease; Alzheimer's disease; epilepsy;  
 KW Leukodystrophy; J14; 14-14-14; 14-14-14; 14-14-14; 14-14-14;  
 KW systemic lupus erythematosus; myocardial infarction; inflammation;  
 KW diagnosis; therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FH Initia 1..22  
 FT /tag= a  
 FT /note= "intron 9 (0.137 Kb) 5' end"  
 FT exon 23..31  
 FT /tag= b  
 FT /note= "exon 10 (71 bp) 5' end"  
 XX  
 PN M09844106-A1.  
 XX  
 P2 02-APR-1999; 99MO 0400972.  
 XX  
 PP 15-MAY-1997; 97MR-0000920.  
 XX  
 PR 03-APR-1997; 97GB-0006731.  
 XX  
 PA (KIDP/) KIDLE S J.  
 PA (NICOD/) NICOD P.  
 PA (WAER/) WAERER G.  
 XX  
 PI Bonny C, Waerber G;  
 XX  
 DP WPI; 1998-56278/48.  
 XX  
 FT New isolated transcription factor islet-brain 1: used to develop  
 FT products for treating e.g. diabetes, neurodegenerative disorders,  
 FT cancers, autoimmune disease, heart disease or epilepsy  
 XX  
 PS Disclosure, Page 77, 11pp; English.  
 XX  
 CC This is the nucleotide sequence of the human IB1 gene, which has been cloned from  
 CC of the human islet-brain 1 (IB1) gene, which has been cloned from  
 CC a bacterial artificial chromosome. Exon-intron boundaries (see  
 CC AAV45556-77) for the human IB1 gene were determined. IB1 is a novel  
 CC transcription factor involved in control of the GUT2 and insulin  
 CC genes. IB1 polypeptides (see AAV45561-92), nucleic acids (see  
 CC AAV45563-64), agonists and antagonists are useful in the treatment  
 CC of diabetes, neurodegenerative diseases such as dementia,  
 CC and/or parkinsonism, the inhibition or promotion of apoptosis, and  
 CC cancer.  
 XX  
 SQ Sequence 31 BP; 6 A; 8 C; 6 G; 11 T; 0 other;  
 Query Match: 57.6%, Score 14.4, E-21, Length 31,  
 Best Local Similarity: 75.0%; Pred. No. 9.1e+03;  
 Matches: 18; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;  
 QY 2 TTTTCTTATATGCTGTTGCTG 24  
 |||||  
 Db 3 TTTTCTTATATGCTGTTGCTG 25  
 RESULT 15  
 AAH25675  
 ID AAH25675 standard, DNA; 20 BP.  
 AC AAH25675;  
 DT 05-SEP-2001 (first entry)









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XX WP1: 1979-009433/01.
XX
XX New Helicobacter pylori antigens and antibodies for diagnosis
XX
XX useful in serological diagnosis of infection of Helicobacter pylori
XX
XX long-lasting immune response
XX
XX Claim Example 5A; Page 209; 400pp; English.
XX
XX
XX The present PCR assay was used to identify patients with gastric
XX
XX encoding a polypeptide of 100 amino acids, the amino acid
XX
XX protein of Helicobacter pylori and antibodies to the protein
XX
XX antisera. The specificities and sensitivities of the antisera
XX
XX immunogenicity studies. Helicobacter pylori antigens are used to
XX
XX H. pylori specific antibodies, for diagnosis of infection of
XX
XX eradication of infection, and in various clinical applications.
XX
XX infection and related diseases (gastroitis, peptic ulcer, gastric
XX
XX adenocarcinoma, lymphoma).
XX
XX Sequence 32 BP; 18 A; 7 C; 6 G; 1 T; 0 other;
XX
XX Query March 60.8%; Score 15.2; EB 20; Length 32;
XX
XX Best Local Similarity 85.0%; Pos 1; Neg 3;
XX
XX Matches 17; Coverage 100%; of Viewed 17; 100% of 17
XX
XX
XX 1 TTTCTTTCTGATGCTGTT 20
XX
XX 31 TTTTCTTCTGTTGGTGT 12
XX
XX
XX RESULT 3
XX
XX AB064556
XX
XX AB064556 standard; DNA; 25 BP.
XX
XX AB064556;
XX
XX 20-AUG-2002 (first entry)
XX
XX
XX Human KTM1A portion (AB063133) Probe # 1469.
XX
XX
XX Human: PROM1A, KTM1A, KIDNEY, LIVER, COLON, PANCREAS, SPLEEN,
XX
XX (Gene Therapy) Cancer, Kidney, Liver, Colon, Pancreas, Spleen,
XX
XX 1999; Human: Human: Kidney, Liver, Colon, Pancreas, Spleen,
XX
XX Homo sapiens.
XX
XX
XX Homo sapiens.
XX
XX
XX WO200224750-A2.
XX
XX
XX 28-MAR-2002.
XX
XX
XX 21-SEP-2001; 2001WG US24656.
XX
XX
XX 21-SEP-2001; 2000HS-2344A/P.
XX
XX 27-SEP-2001; 2000HS-236359P.
XX
XX 04-OCT-2000; 2000SP-0024262.
XX
XX 30-JAN-2001; 2001W-0300661.
XX
XX 30-JAN-2001; 2001W-0300662.
XX
XX 30-JAN-2001; 2001W-0300663.
XX
XX 30-JAN-2001; 2001W-0300664.
XX
XX 30-JAN-2001; 2001W-0300665.
XX
XX 30-JAN-2001; 2001W-0300666.
XX
XX 30-JAN-2001; 2001W-0300667.
XX
XX 30-JAN-2001; 2001W-0300668.
XX
XX 30-JAN-2001; 2001W-0300669.
XX
XX 28-MAR-2001; 2001W-0300670.
XX
XX
XX (AEOM ) AECMICA INC.
XX
XX Zhang J.
XX
XX WP1: 2002-479509/51.
XX
XX

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[illegible]







C 667	11.2	44.8	32	21	AAH51754	Isoterm-specific F	740	11	44.0	21	24	AAH51735	Reverse transcriptase	Human actin
C 668	11.2	44.8	32	22	AAH51754	Oligonucleotide #8	741	11	44.0	22	25	AAH51735	Reverse transcriptase	Human actin
C 669	11.2	44.8	32	24	AAH51754	Human factor VIII	742	11	44.0	24	26	AAH51735	Reverse transcriptase	Human actin
C 670	11.2	44.8	33	19	AAH51754	5' nested primer F	743	11	44.0	19	15	AAH51735	Reverse transcriptase	Human actin
C 671	11.2	44.8	33	19	AAH51754	Cfi-1 binding site	744	11	44.0	19	15	AAH51735	Reverse transcriptase	Human actin
C 672	11.2	44.8	33	22	AAH51754	Human VEGF-A reverb	745	11	44.0	22	17	AAH51735	Reverse transcriptase	Human actin
C 673	11.2	44.8	33	22	AAH51754	Human ribosomal si	746	11	44.0	22	19	AAH51735	Reverse transcriptase	Human actin
C 674	11.2	44.8	33	24	AAH51754	Insulin-like growth	747	11	44.0	24	20	AAH51735	Reverse transcriptase	Human actin
C 675	11.2	44.8	32	24	AAH51754	Human ubiquitin	748	11	44.0	24	20	AAH51735	Reverse transcriptase	Human actin
C 676	11.2	44.8	34	22	AAH51754	Human inflammatory	749	11	44.0	22	20	AAH51735	Reverse transcriptase	Human actin
C 677	11.2	44.8	34	22	AAH51754	Non-endogenous hum	750	11	44.0	22	20	AAH51735	Reverse transcriptase	Human actin
C 678	11.2	44.8	34	23	AAH51754	HIV env INS mutagen	751	11	44.0	23	20	AAH51735	Reverse transcriptase	Human actin
C 679	11.2	44.8	35	14	AAH51754	PCR primer for hum	752	11	44.0	14	20	AAH51735	Reverse transcriptase	Human actin
C 680	11.2	44.8	35	14	AAH51754	Oligonucleotide F1	753	11	44.0	14	20	AAH51735	Reverse transcriptase	Human actin
C 681	11.2	44.8	12	23	AAH51754	Oligonucleotide F1	754	11	44.0	23	15	AAH51735	Reverse transcriptase	Human actin
C 682	11.2	44.8	12	23	AAH51754	Oligonucleotide F1	755	11	44.0	23	15	AAH51735	Reverse transcriptase	Human actin
C 683	11.2	44.8	13	23	AAH51754	Oligonucleotide SE	756	11	44.0	23	17	AAH51735	Reverse transcriptase	Human actin
C 684	11.2	44.8	13	23	AAH51754	Oligonucleotide SE	757	11	44.0	23	19	AAH51735	Reverse transcriptase	Human actin
C 685	11.2	44.8	13	23	AAH51754	Oligonucleotide SE	758	11	44.0	23	20	AAH51735	Reverse transcriptase	Human actin
C 686	11.2	44.8	13	23	AAH51754	Oligonucleotide SE	759	11	44.0	23	22	AAH51735	Reverse transcriptase	Human actin
C 687	11.2	44.8	13	23	AAH51754	Sequence used in n	760	11	44.0	23	22	AAH51735	Reverse transcriptase	Human actin
C 688	11.2	44.8	15	18	AAH51754	Mass spectrometric	761	11	44.0	15	17	AAH51735	Reverse transcriptase	Human actin
C 689	11.2	44.8	15	19	AAH51754	Respiratory syncyt	762	11	44.0	15	17	AAH51735	Reverse transcriptase	Human actin
C 690	11.2	44.8	15	22	AAH51754	HTG22 allele spec	763	11	44.0	15	17	AAH51735	Reverse transcriptase	Human actin
C 691	11.2	44.8	15	22	AAH51754	Human G-protein-co	764	11	44.0	15	17	AAH51735	Reverse transcriptase	Human actin
C 692	11.2	44.8	15	24	AAH51754	Human TIE-2 subst	765	11	44.0	15	17	AAH51735	Reverse transcriptase	Human actin
C 693	11.2	44.8	17	20	AAH51754	Human C-raf target	766	11	44.0	17	20	AAH51735	Reverse transcriptase	Human actin
C 694	11.2	44.8	17	20	AAH51754	Human C-raf target	767	11	44.0	17	20	AAH51735	Reverse transcriptase	Human actin
C 695	11.2	44.8	17	20	AAH51754	Human C-raf target	768	11	44.0	17	20	AAH51735	Reverse transcriptase	Human actin
C 696	11.2	44.8	17	20	AAH51754	Human C-raf target	769	11	44.0	17	20	AAH51735	Reverse transcriptase	Human actin
C 697	11.2	44.8	17	20	AAH51754	Human C-raf target	770	11	44.0	17	20	AAH51735	Reverse transcriptase	Human actin
C 698	11.2	44.8	17	20	AAH51754	Human C-raf target	771	11	44.0	17	20	AAH51735	Reverse transcriptase	Human actin
C 699	11.2	44.8	17	20	AAH51754	Human C-raf target	772	11	44.0	17	20	AAH51735	Reverse transcriptase	Human actin
C 700	11.2	44.8	17	22	AAH51754	Factor VIII mutati	773	11	44.0	17	22	AAH51735	Reverse transcriptase	Human actin
C 701	11.2	44.8	19	21	AAH51754	Human beta-tubulin	774	11	44.0	19	21	AAH51735	Reverse transcriptase	Human actin
C 702	11.2	44.8	19	21	AAH51754	Mouse IPR-gamma #1	775	11	44.0	19	21	AAH51735	Reverse transcriptase	Human actin
C 703	11.2	44.8	19	21	AAH51754	Human gene sligapu	776	11	44.0	19	21	AAH51735	Reverse transcriptase	Human actin
C 704	11.2	44.8	20	16	AAH51754	Chromosome 11 (loc	777	11	44.0	20	16	AAH51735	Reverse transcriptase	Human actin
C 705	11.2	44.8	20	16	AAH51754	Glycylamyl inducin	778	11	44.0	20	16	AAH51735	Reverse transcriptase	Human actin
C 706	11.2	44.8	20	19	AAH51754	Antisense oligonuc	779	11	44.0	20	19	AAH51735	Reverse transcriptase	Human actin
C 707	11.2	44.8	20	20	AAH51754	PCR primer used to	780	11	44.0	20	20	AAH51735	Reverse transcriptase	Human actin
C 708	11.2	44.8	20	20	AAH51754	PCR primer used to	781	11	44.0	20	20	AAH51735	Reverse transcriptase	Human actin
C 709	11.2	44.8	20	20	AAH51754	PCR primer used to	782	11	44.0	20	20	AAH51735	Reverse transcriptase	Human actin
C 710	11.2	44.8	20	20	AAH51754	PCR primer used to	783	11	44.0	20	20	AAH51735	Reverse transcriptase	Human actin
C 711	11.2	44.8	20	20	AAH51754	PCR primer used to	784	11	44.0	20	20	AAH51735	Reverse transcriptase	Human actin
C 712	11.2	44.8	20	21	AAH51754	Non-B, non-C, non-	785	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 713	11.2	44.8	20	21	AAH51754	Human beta-tubulin	786	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 714	11.2	44.8	20	21	AAH51754	Human beta-tubulin	787	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 715	11.2	44.8	20	21	AAH51754	Human beta-tubulin	788	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 716	11.2	44.8	20	21	AAH51754	Human beta-tubulin	789	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 717	11.2	44.8	20	21	AAH51754	Human beta-tubulin	790	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 718	11.2	44.8	20	21	AAH51754	Human beta-tubulin	791	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 719	11.2	44.8	20	21	AAH51754	Human beta-tubulin	792	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 720	11.2	44.8	20	21	AAH51754	Human beta-tubulin	793	11	44.0	20	21	AAH51735	Reverse transcriptase	Human actin
C 721	11.2	44.8	20	22	AAH51754	Human beta-tubulin	794	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 722	11.2	44.8	20	22	AAH51754	Human beta-tubulin	795	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 723	11.2	44.8	20	22	AAH51754	Human beta-tubulin	796	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 724	11.2	44.8	20	22	AAH51754	Human beta-tubulin	797	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 725	11.2	44.8	20	22	AAH51754	Human beta-tubulin	798	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 726	11.2	44.8	20	22	AAH51754	Human beta-tubulin	799	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 727	11.2	44.8	20	22	AAH51754	Human beta-tubulin	800	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 728	11.2	44.8	20	22	AAH51754	Human beta-tubulin	801	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 729	11.2	44.8	20	22	AAH51754	Human beta-tubulin	802	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 730	11.2	44.8	20	22	AAH51754	Human beta-tubulin	803	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 731	11.2	44.8	20	22	AAH51754	Human beta-tubulin	804	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 732	11.2	44.8	20	22	AAH51754	Human beta-tubulin	805	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 733	11.2	44.8	20	22	AAH51754	Human beta-tubulin	806	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 734	11.2	44.8	20	22	AAH51754	Human beta-tubulin	807	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 735	11.2	44.8	20	22	AAH51754	Human beta-tubulin	808	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 736	11.2	44.8	20	22	AAH51754	Human beta-tubulin	809	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 737	11.2	44.8	20	22	AAH51754	Human beta-tubulin	810	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 738	11.2	44.8	20	22	AAH51754	Human beta-tubulin	811	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin
C 739	11.2	44.8	20	22	AAH51754	Human beta-tubulin	812	11	44.0	20	22	AAH51735	Reverse transcriptase	Human actin

[illegible]











DN 23 TTTCTTTCTGTGATGTGTG 1

RESULT 46  
ARI70667/2 31 bp DNA linear PAT 17 DEC-2001

LOCUS ARI70667  
DEFINITION Sequence 101 from Patent US 6291664.  
ACCESSION ARI70667  
VERSION ARI70667.1 GI:17908626  
KEYWORDS

SOURCE  
ORGANISM

REFERENCE  
1 (bases 1 to 31)  
Unclassified.

AUTHORS Pavlakis G.N. and Folber P.K.  
TITLE Method of identifying inhibitory/regulatory regions of RNA  
JOURNAL Patent: US 6291664-A 101 18 SEP 2001;  
FEATURES  
Location/Qualifiers  
1..31  
source /organism="unknown"

BASE COUNT 17 a 7 c 3 g 4 t  
ORIGIN

Query Match 93.6%, Score 13.4, DP 6; Length 31;  
Best Local Similarity 73.9%; P-adj. No. 2.6e+05;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TTTCTTTCTGTGATGTGTG 24  
DN 23 TTTCTTTCTGTGATGTGTG 1

Search completed: July 21, 2003, 14:35:22  
Job time : 265.581 secs



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RESULT 35
LOCUS 177011
DEFINITION 24 Jan 97: from patent US 5633472.
ACCESSION 177011
VERSION 177011.1 GI:1031865
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Shattuck-Schlag, C.M., Chumak, J., D'Amico, F., Emil, M. and Nakamura, Y.
TITLE Linker protein and ovarian cancer susceptibility gene
JOURNAL Patent: US 5633472-A 71 02-DEC-1997;
FEATURES
Source 1..30
/organism="Unknown"

BASE COUNT 5 a 6 c 4 g 15 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 30
Best Local Similarity 80.0% Prod. No. 2.6e+05
Matches 16/ Conservative 0/ Mismatches 4/ Indels 0/ Gaps 0/

QY 1 TTTTTCATATGCTGTT 20
Db 8 TTTTTCATATGCTGTT 27

RESULT 36
LOCUS 181006
DEFINITION Sequence 71 from Patent US 5700443.
ACCESSION 181006
VERSION 181006.1 GI:1209206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Shattuck-Schlag, C.M., Sward, J., Durocher, F., Emil, M. and Nakamura, Y.
TITLE Linker protein and ovarian cancer susceptibility gene
JOURNAL Patent: US 5700443-A 71 20-JAN-1998;
FEATURES
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BASE COUNT 5 a 6 c 4 g 15 t
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Best Local Similarity 80.0% Prod. No. 2.6e+05
Matches 16/ Conservative 0/ Mismatches 4/ Indels 0/ Gaps 0/

QY 1 TTTTTCATATGCTGTT 20
Db 8 TTTTTCATATGCTGTT 27

RESULT 37
LOCUS 181102
DEFINITION Sequence 71 from Patent US 5710091.
ACCESSION 181102
VERSION 181102.1 GI:1209392
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Shattuck-Schlag, C.M., Sward, J., Durocher, F., Emil, M. and Nakamura, Y.
TITLE Linker protein and ovarian cancer susceptibility gene
JOURNAL Patent: US 5710091-A 71 20-JAN-1998;
FEATURES
Source 1..30
/organism="Unknown"

BASE COUNT 5 a 6 c 4 g 15 t
ORIGIN
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Best Local Similarity 80.0% Prod. No. 2.6e+05
Matches 16/ Conservative 0/ Mismatches 4/ Indels 0/ Gaps 0/

QY 1 TTTTTCATATGCTGTT 20
Db 8 TTTTTCATATGCTGTT 27

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TITLE and Furell, P. Andrew.
JOURNAL 17q linked breast and ovarian cancer susceptibility gene
PATENT: US 5710091-A 71 20 JAN-1998;
FEATURES
Source 1..30
/organism="Unknown"

BASE COUNT 5 a 6 c 4 g 15 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 30
Best Local Similarity 80.0% Prod. No. 2.6e+05
Matches 16/ Conservative 0/ Mismatches 4/ Indels 0/ Gaps 0/

QY 1 TTTTTCATATGCTGTT 20
Db 8 TTTTTCATATGCTGTT 27

RESULT 38
LOCUS AP079777/c
DEFINITION Sequence 101 from Patent US 5665726.
ACCESSION AP079777
VERSION AP079777.1 GI:1006619
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS Pavlakis, G.N. and Felber, P.K.
TITLE Method of eliminating inhibitory/instability regions of DNA
JOURNAL Patent: US 5665726-A 70 12 OCT-1993;
FEATURES
Source 1..31
/organism="Unknown"

BASE COUNT 17 a 7 c 3 g 4 t
ORIGIN
Query Match 53.6% Score 13.4 DB 6 Length 31
Best Local Similarity 73.9% Prod. No. 2.6e+05
Matches 17/ Conservative 0/ Mismatches 6/ Indels 0/ Gaps 0/

QY 1 TTTTTCATATGCTGTTG 24
Db 23 TTTTTCATATGCTGTTG 1

RESULT 39
LOCUS AP081307/c
DEFINITION Sequence 101 from Patent US 5972596.
ACCESSION AP081307
VERSION AP081307.1 GI:1009033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS Pavlakis, G.N. and Felber, P.K.
TITLE Nucleic acid constructs containing HIV genes with mutation inhibitory/instability regions and methods of using same
JOURNAL Patent: US 5972596-A 70 26 OCT-1994;
FEATURES
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/organism="Unknown"

BASE COUNT 17 a 7 c 3 g 4 t
ORIGIN
Query Match 53.6% Score 13.4 DB 6 Length 31
Best Local Similarity 73.9% Prod. No. 2.6e+05
Matches 17/ Conservative 0/ Mismatches 6/ Indels 0/ Gaps 0/

QY 1 TTTTTCATATGCTGTTG 24
Db 23 TTTTTCATATGCTGTTG 24

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AUTHORS: Watanabe, P.J. and Wong, K.C.  
 TITLE: Primers for identifying typing or classifying nucleic acids  
 JOURNAL: WO 00/00044-A 523 32 27-V-2000  
 Amersham Pharmacia Biotech AB (SE)  
 FEATURES: location/Qualifiers  
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 /db\_xref="taxon:32630"  
 /note="16S rRNA Homology Primer Sequence"  
 BASE COUNT 1 a 4 c 4 g 16 t  
 ORIGIN  
 Query Match 54.4% Score 13.6; DB 6; Length 25;  
 Best Local Similarity 80.0%; Fwd. Hc. 2.2e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0  
 1 TTCTTTCTATGCTGCTT 20  
 3 TTTTCTTTGCTGCTGCTT 22  
 RESULT 31  
 LOCUS: AM043016 45 bp LNA linear PAT 21-NOV-2000  
 DEFINITION: Sequence for identifying typing or classifying nucleic acids  
 AM043016  
 VERSION: AM043016.1 GI 11141624  
 KEYWORDS: synthetic construct, synthetic construct, artificial sequences.  
 ORIGIN  
 REFERENCE 1 (bases 1 to 25)  
 AUTHORS: Watanabe, P.J. and Wong, K.C.  
 TITLE: Primers for identifying typing or classifying nucleic acids  
 JOURNAL: WO 00/00044-A 523 32 27-V-2000  
 Amersham Pharmacia Biotech AB (SE)  
 FEATURES: location/Qualifiers  
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 /db\_xref="taxon:32630"  
 /note="16S rRNA Homology Primer Sequence"  
 BASE COUNT 2 a 1 c 3 g 19 t  
 ORIGIN  
 Query Match 54.4% Score 13.6; DB 6; Length 25;  
 Best Local Similarity 80.0%; Fwd. Hc. 2.2e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0  
 1 TTCTTTCTATGCTGCTT 20  
 6 TTTTCTTTGCTGCTGCTT 25  
 RESULT 32  
 LOCUS: AM044741 30 bp DNA linear PAT 04-DEC-1998  
 DEFINITION: Sequence 71 from patent US 5,747,252.  
 AM044741  
 VERSION: AM044741.1 GI 19414729  
 KEYWORDS: Unknown.  
 ORIGIN: Unknown.  
 REFERENCE: 1 (bases 1 to 30)  
 AUTHORS: Skolnick, M.H., Goldgar, D.E., Mikl, Y., Swenson, J., Karb, A.,  
 and Futreal, P. Andrew.  
 TITLE: 170-linked breast and ovarian cancer susceptibility gene  
 JOURNAL: US 5,747,252-A 71 05-MAY-1998;  
 FEATURES: location/Qualifiers  
 source 1..30  
 /organism="unknown"  
 BASE COUNT 5 a 6 c 4 g 15 t

ORIGIN  
 Query Match 54.4% Score 13.6; DB 6; Length 30;  
 Best Local Similarity 80.0%; Fwd. Hc. 2.2e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0  
 1 TTCTTTCTATGCTGCTT 20  
 8 TGCTTTCTATGCTGCTT 27  
 RESULT 33  
 LOCUS: AR068227 30 bp DNA linear PAT 04-DEC-1998  
 DEFINITION: Sequence 71 from patent US 5,753,441.  
 AR068227  
 VERSION: AR068227.1 GI:3967336  
 KEYWORDS: Unknown.  
 ORIGIN: Unknown.  
 REFERENCE: 1 (bases 1 to 30)  
 AUTHORS: Skolnick, M.H., Goldgar, D.E., Mikl, Y., Swenson, J., Karb, A.,  
 Harsman, K.D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.,  
 and Futreal, P. Andrew.  
 TITLE: 170-linked breast and ovarian cancer susceptibility gene  
 JOURNAL: US 5,753,441-A 71 10-MAY-1998;  
 FEATURES: location/Qualifiers  
 source 1..30  
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 BASE COUNT 5 a 6 c 4 g 15 t  
 ORIGIN  
 Query Match 54.4% Score 13.6; DB 6; Length 30;  
 Best Local Similarity 80.0%; Fwd. Hc. 2.2e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0  
 1 TTCTTTCTATGCTGCTT 20  
 8 TGCTTTCTATGCTGCTT 27  
 RESULT 34  
 LOCUS: AR137010 30 bp DNA linear PAT 16-NOV-2001  
 DEFINITION: Sequence 71 from patent US 6,162,897.  
 AR137010  
 VERSION: AR137010.1 GI:11478263  
 KEYWORDS: Unknown.  
 ORIGIN: Unknown.  
 REFERENCE: 1 (bases 1 to 30)  
 AUTHORS: Skolnick, M.H., Goldgar, D.E., Mikl, Y., Swenson, J., Karb, A.,  
 Skolnick, M.H., Goldgar, D.E., Mikl, Y., Swenson, J., Karb, A.,  
 Harsman, K.D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.,  
 and Futreal, P. Andrew.  
 TITLE: 170-linked breast and ovarian cancer susceptibility gene  
 JOURNAL: US 6,162,897-A 71 16-NOV-2000;  
 FEATURES: location/Qualifiers  
 source 1..30  
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 BASE COUNT 5 a 6 c 4 g 15 t  
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 Query Match 54.4% Score 13.6; DB 6; Length 30;  
 Best Local Similarity 80.0%; Fwd. Hc. 2.2e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0  
 1 TTCTTTCTATGCTGCTT 20  
 8 TGCTTTCTATGCTGCTT 27

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ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 22
Best Local Similarity 89.2% Fred. No. 126055
Matches 16 Conservative 0 Mismatches 0 Indels 0 Gaps 0
1 TTTCTTTCTATGCTCT 17
1 TTTCTTTCTATGCTCT 25

Db 9 TTTCTTTCTATGCTCT 25

RESULT 26
AX042956 25 bp DNA linear PAT 24 NOV 2000
LOCUS AX042956
DEFINITION Sequence 254 from Patent WO0065088.
ACCESSION AX042956
VERSION AX042956.1 GI:11341604
KEYWORDS
SOURCE
ORGANISM human.
REFERENCE
AUTHORS Zhang, J.
TITLE Human vitronectin cytochrome c oxidase protein 1
JOURNAL Patent WO 0044750 A 1940 24 MAR 2002;
Acemica, Inc. (US)
FEATURES
source
location/Qualifiers
1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 6 a 6 c 5 g 8 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 22
Best Local Similarity 89.2% Fred. No. 126055
Matches 16 Conservative 0 Mismatches 0 Indels 0 Gaps 0
2 TTTCTTTCTATGCTCT 18
1 TTTCTTTCTATGCTCT 17

RESULT 27
AR066675 16 bp DNA linear PAT 20 SEP 1998
LOCUS AR066675
DEFINITION Sequence 21 from Patent US 5851760.
ACCESSION AR066675
VERSION AR066675.1 GI:15977897
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Evans, C.A. and Smith, M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent US 5851760-A 23 22-DEC-1998;
location/Qualifiers
1..22
source
/organism="Unknown"

BASE COUNT 14 a 6 c 1 g 1 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 22
Best Local Similarity 89.2% Fred. No. 126055
Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0
1 TTTCTTTCTATGCTCT 24
22 TTTCTTTCTATGCTCT 3

RESULT 28

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AA0478/c 24 bp DNA linear PAT 24 NOV 2000
LOCUS AA0478
DEFINITION Sequence 224 from Patent WO0065088.
ACCESSION AA0478
VERSION AA0478.1 GI:11341604
KEYWORDS
SOURCE
ORGANISM unidentified.
REFERENCE
AUTHORS Tarin, D. and Matsumura, Y.
TITLE Diagnostic Method AND PCR
JOURNAL Patent WO 0045728 A 1998-11-19;
1315 (EN:ACTION 05B)
FEATURES
source
location/Qualifiers
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/db_xref="taxon:12644"

BASE COUNT 9 a 7 c 6 g 2 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 24
Best Local Similarity 89.0% Fred. No. 226055
Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0
1 TTTCTTTCTATGCTCT 25
24 TTTCTTTCTATGCTCT 5

RESULT 29
AX042958 25 bp DNA linear PAT 24 NOV 2000
LOCUS AX042958
DEFINITION Sequence 524 from Patent WO0065088.
ACCESSION AX042958
VERSION AX042958.1 GI:11341604
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE
AUTHORS Ullendahl, P. J. and Wang, R. C.
TITLE Primers for identifying typing of clonally derived human cells
JOURNAL Patent WO 0065088 A 524 02 NOV 2000;
Ametech Pharmacia Biotech AB (SE)
FEATURES
source
location/Qualifiers
1..25
/organism="synthetic construct"
/db_xref="taxon:12630"
/note="16S rRNA Homozygote Primer Sequence"

BASE COUNT 3 a 1 c 3 g 19 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 20
Best Local Similarity 89.0% Fred. No. 226055
Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0
1 TTTCTTTCTATGCTCT 20
5 TTTCTTTCTATGCTCT 24

RESULT 30
AX042956 25 bp DNA linear PAT 24 NOV 2000
LOCUS AX042956
DEFINITION Sequence 524 from Patent WO0065088.
ACCESSION AX042956
VERSION AX042956.1 GI:11341604
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE
AUTHORS Ullendahl, P. J. and Wang, R. C.
TITLE Primers for identifying typing of clonally derived human cells
JOURNAL Patent WO 0065088 A 524 02 NOV 2000;
Ametech Pharmacia Biotech AB (SE)
FEATURES
source
location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:12630"
/note="16S rRNA Homozygote Primer Sequence"

BASE COUNT 3 a 1 c 3 g 19 t
ORIGIN

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AX476133  
LOCUS AX476133 17 bp DNA linear EST 12 AUG 2002  
DEFINITION Sequence 174 bp from cDNA, 5' end  
ACCESSION AX476133  
VERSION AX476133.1 GI:22214446  
KEYWORDS  
SOURCE human  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Zhang, J.  
TITLE Human kidney tumor overexpressed membrane protein 1  
JOURNAL J. Biol. Chem. 278(44):42442-42446, 2003  
AECOMICA, INC. (US)  
FEATURES  
SOURCE location/Qualifiers  
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/db\_xref="taxon:9606"  
BASE COUNT 1 a 4 c 3 g 9 t  
ORIGIN

Query Match 55.2% Score 13.87 E-6 Length 17  
Best Local Similarity 55.2% E-6 Length 17  
Matches 15, Conservation 2, Indels 0, Gaps 0

CV 1 TTCTTTCTGATGCT 17  
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1 TTCTCTTCATGATGCT 17

RESULT 22  
AX475134 17 bp DNA linear EST 12 AUG 2002  
LOCUS AX475134  
DEFINITION Sequence 395 bp from cDNA, 5' end  
ACCESSION AX475134  
VERSION AX475134.1 GI:22214419  
KEYWORDS  
SOURCE human  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Zhang, J.  
TITLE Human kidney tumor overexpressed membrane protein 1  
JOURNAL J. Biol. Chem. 278(44):42442-42446, 2003  
AECOMICA, INC. (US)  
FEATURES  
SOURCE location/Qualifiers  
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BASE COUNT 1 a 4 c 4 g 8 t  
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Matches 15, Conservation 2, Indels 0, Gaps 0

CV 2 TTCTTTCTGATGCT 18  
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1 TTCTCTTCATGATGCT 17

RESULT 23  
AR178914/c 21 bp DNA linear EST 12 AUG 2002  
LOCUS AR178914/c  
DEFINITION Sequence 100 bp from cDNA, 5' end  
ACCESSION AR178914  
VERSION AR178914.1 GI:22214419  
KEYWORDS  
SOURCE unknown  
ORGANISM unknown  
Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Demetriou, C., and Vickers, T.A.  
TITLE Identification of peptides and methods for the isolation of the  
expression of R protein  
JOURNAL J. Biol. Chem. 276(44):42442-42446, 2001  
AECOMICA, INC. (US)  
FEATURES  
SOURCE location/Qualifiers  
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ORIGIN

Query Match 55.2% Score 13.87 E-6 Length 20  
Best Local Similarity 55.2% E-6 Length 20  
Matches 17, Conservation 2, Indels 0, Gaps 0

CV 2 TTCTTTCTGATGCT 18  
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1 TTCTCTTCATGATGCT 17

RESULT 24  
AX043229 25 bp DNA linear EST 12 AUG 2002  
LOCUS AX043229  
DEFINITION Sequence 140 bp from cDNA, 5' end  
ACCESSION AX043229  
VERSION AX043229.1 GI:11341837  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
AUTHORS Ulfendahl, P., and Wong, K.C.  
TITLE Primers for identifying typing of classifying nucleic acids  
JOURNAL J. Biol. Chem. 276(44):42442-42446, 2001  
AECOMICA, INC. (US)  
FEATURES  
SOURCE location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:13630"  
/note="CDR1 Heredity/lytic Filtered Sequence"  
BASE COUNT 3 a 3 c 4 g 15 t  
ORIGIN

Query Match 55.2% Score 13.87 E-6 Length 25  
Best Local Similarity 55.2% E-6 Length 25  
Matches 15, Conservation 2, Indels 0, Gaps 0

CV 1 TTCTTTCTGATGCT 25  
|||||  
1 TTCTTTCTGATGCT 25

RESULT 25  
AX476110 26 bp DNA linear EST 12 AUG 2002  
LOCUS AX476110  
DEFINITION Sequence 100 bp from cDNA, 5' end  
ACCESSION AX476110  
VERSION AX476110.1 GI:22214419  
KEYWORDS  
SOURCE human  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Zhang, J.  
TITLE Human kidney tumor overexpressed membrane protein 1  
JOURNAL J. Biol. Chem. 278(44):42442-42446, 2003  
AECOMICA, INC. (US)  
FEATURES  
SOURCE location/Qualifiers  
1..25  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 3 a 6 c 5 g 11 t  
ORIGIN



SYNTHETIC	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences
PRYMPONS	WO 0190557 A1

DEFINITION Sequence 1188 from Patent WO0224490.  
 ACCESSION AX476117  
 VERSION AX476117.1 GI:22215402  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi; Mammalia; Primates; Carnivora; Hominoidea; Homo

REFERENCE  
 AUTHORS Zhang, J.  
 TITLE Human kidney tumor overexpressed membrane protein 1  
 JOURNAL Patent: WO 0224/50 A 139 28 MAR 2002;  
 Accutec, Inc. (US)  
 FEATURES  
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Query Match  
 Best Local Similarity 59.2% Score 14.8; DB 6; Length 25;  
 Best Local Similarity 99.9%; Pred. No. 6.5e+04;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Cy  
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Db  
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RESULT 9  
 LOCUS AX476118 25 bp DNA linear PAT 12 NOV 2002  
 DEFINITION Sequence 1198 from Patent WO0224490.  
 ACCESSION AX476118  
 VERSION AX476118.1 GI:22215403  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi; Mammalia; Primates; Carnivora; Hominoidea; Homo

REFERENCE  
 AUTHORS Zhang, J.  
 TITLE Human kidney tumor overexpressed membrane protein 1  
 JOURNAL Patent: WO 0224/50 A 139 28 MAR 2002;  
 Accutec, Inc. (US)  
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 source location/Qualifiers  
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BASE COUNT  
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ORIGIN  
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 2

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 Best Local Similarity 99.9%; Pred. No. 6.5e+04;  
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Cy  
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Db  
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 2 TTTCTTTCTGATGCTG 19

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 LOCUS A11317 25 bp DNA linear PAT 03 NOV 1995  
 DEFINITION oligonucleotide from Patent EP0411119.  
 ACCESSION A11317  
 VERSION A11317.1 GI:1249339  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM artificial sequences  
 1 (bases 1 to 25)  
 AUTHORS Singh, M. and Thomas, J.

TITLE Hybrid protein for the 16 kDa antigen from W. reovirus, E. coli as host, the 38 kDa antigen and a 3 kDa protein  
 JOURNAL Patent: EP 0619019 A 4 24 Feb 1992;  
 Gesellschaft für Biotechnologische Forschung mbH (GBF)  
 FEATURES  
 source location/Qualifiers  
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Db  
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 2 TTTCTTTCTGATGCTG 22

RESULT 11  
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 DEFINITION Sequence 1023 from Patent W00065088.  
 ACCESSION AX043457  
 VERSION AX043457.1 GI:11342065  
 KEYWORDS  
 SOURCE synthetic construct,  
 ORGANISM artificial construct.  
 1 (bases 1 to 25)  
 AUTHORS Hirschfeld, P. J. and Wong, K. C.  
 TITLE Plasmid for identifying and classifying nucleic acids  
 JOURNAL Patent: W0 0065088 A 1004 01 Nov 2000;  
 Amer sham Biotech AB (US)  
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 /db\_xref="taxon:32630"  
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Query Match  
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Db  
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RESULT 12  
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 DEFINITION Sequence 2 from Patent W09713974.  
 ACCESSION A62421  
 VERSION A62421.1 GI:1716353  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 1 (bases 1 to 31)  
 AUTHORS Weindl, K.  
 TITLE METHOD OF IDENTIFYING A STRAIN OF THE GENUS  
 JOURNAL PATENT: WO 97/0874 A 4 17 APR 1997;  
 BOEHRINGER MANNHEIM GMBH (DE)  
 OTHER PUBLICATIONS DE 1947952 970417.  
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 /db\_xref="taxon:32644"

BASE COUNT  
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source 1.25

/db\_xref="taxon:9606"

BASE COUNT 2 a 7 c 5 g 11 t

Query Match

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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGTCG 18

DB 7 TTTCTTGCATGTCG 24

RESULT 4

AX476113

LOCUS AX476113 25 bp DNA linear FAT 12 AUG 2002

DEFINITION Sequence 1337 from Patent WO0224750.

ACCESSION AX476113

VERSION 1.0

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TIME

JOURNAL

FEATURES

source

BASE COUNT 3 a 6 c 5 g 11 t

ORIGIN

Query Match

Best Local Similarity 89.28; Score 14.8; Db 6; Length 25;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGTCG 18

DB 6 TTTCTTGCATGTCG 23

RESULT 5

AX476114

LOCUS AX476114 25 bp DNA linear FAT 12 AUG 2002

DEFINITION Sequence 1337 from Patent WO0224750.

ACCESSION AX476114

VERSION 1.0

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TIME

JOURNAL

FEATURES

source

BASE COUNT 3 a 6 c 5 g 10 t

ORIGIN

Query Match

Best Local Similarity 89.28; Score 14.8; Db 6; Length 25;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGTCG 18

DB 5 TTTCTTGCATGTCG 22

RESULT 6

AX476115

LOCUS AX476115 25 bp DNA linear FAT 12 AUG 2002

DEFINITION Sequence 1337 from Patent WO0224750.

ACCESSION AX476115

VERSION 1.0

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TIME

JOURNAL

FEATURES

source

BASE COUNT 4 a 6 c 5 g 9 t

ORIGIN

Query Match

Best Local Similarity 89.28; Score 14.8; Db 6; Length 25;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGTCG 18

DB 4 TTTCTTGCATGTCG 21

RESULT 7

AX476116

LOCUS AX476116 25 bp DNA linear FAT 12 AUG 2002

DEFINITION Sequence 1337 from Patent WO0224750.

ACCESSION AX476116

VERSION 1.0

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TIME

JOURNAL

FEATURES

source

BASE COUNT 5 a 5 c 6 g 9 t

ORIGIN

Query Match

Best Local Similarity 89.28; Score 14.8; Db 6; Length 25;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 3 TTTCTTGCATGTCG 20

RESULT 8

AX476117

LOCUS AX476117 25 bp DNA linear FAT 12 AUG 2002



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 DEFINITION Sequence 6 from Patent W00044409.  
 ACCESSION AX012828  
 VERSION AX012828.1  
 KEYWORDS  
 SOURCE Synthetic construct.  
 ORGANISM Synthetic construct

REFERENCE	Artificial sequences.
AUTHORS	Becker, D. B. and Green, C. R.
TITLE	Formulations comprising antisense nucleotides for treatment of cancer
ABSTRACT	Parent: W0044409-A 1 (1999-01-20)
DESCRIPTION	HEPES (DAVID LAFRANCE, ERIE, ONTARIO, CANADA) (1999-01-20)
FEATURES	Location/Qualifiers
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LOCUS	AX012828
DEFINITION	Sequence 6 from Patent W00044409.
ACCESSION	AX012828
VERSION	AX012828.1
KEYWORDS	
SOURCE	human.
ORGANISM	Human sapiens
REFERENCE	Eukaryotic, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	Zhang, D.
TITLE	Human kidney tumor overexpressed membrane protein 1
ABSTRACT	Parent: W0044409-A 1 (1999-01-20)
DESCRIPTION	Acemica, Inc. (US)
FEATURES	Location/Qualifiers
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DEFINITION	Sequence 6 from Patent W00044409.
ACCESSION	AX012828
VERSION	AX012828.1
KEYWORDS	
SOURCE	human.
ORGANISM	Human sapiens
REFERENCE	Eukaryotic, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	Zhang, D.
TITLE	Human kidney tumor overexpressed membrane protein 1
ABSTRACT	Parent: W0044409-A 1 (1999-01-20)
DESCRIPTION	Acemica, Inc. (US)
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DEFINITION	Sequence 6 from Patent W00044409.
ACCESSION	AX012828
VERSION	AX012828.1
KEYWORDS	
SOURCE	human.
ORGANISM	Human sapiens
REFERENCE	Eukaryotic, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	Zhang, D.
TITLE	Human kidney tumor overexpressed membrane protein 1
ABSTRACT	Parent: W0044409-A 1 (1999-01-20)
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ORIGIN	1..25

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[illegible]

[illegible]

[illegible]



## SUMMARIES

(without alignments)  
280 500 1000 2000 4000 8000 16000

[illegible]

Table 1. *Continued*

Total number of bills satisfying above conditions: 66855

Post-processing:	Minimum Match	0%
------------------	---------------	----

Maximum Match	100%
Listing first 1000 employees	

Tabasco

```

1: gb_ha:*
2: gb_hig:*
3: gb_in:*
4: gb_or:*
5: gb_ow:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pli:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ori:*
22: em_ow:*
23: em_pat:*
24: em_ph:*
25: em_pli:*
26: em_pli:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hig_hum:*
31: em_hig_inv:*
32: em_hig_other:*
33: em_hig_mus:*
34: em_hig_pli:*
35: em_hig_pod:*
36: em_hig_mam:*
37: em_hig_vli:*
38: em_hig_vli:*
39: em_vli_hum:*
40: em_hig_mus:*
41: em_hig_other:*

```

Prod. No. is the number of small fish at 1 yr. known to have

score greater than or equal to the score of the result being printed and is corrected by analysis of the total score distribution.

Result No.	Score	Query Match	length	DB	ID	Description
1	25	100.0	25	6	AA032828	AA032828 Sequence
2	14.9	59.12	25	6	AA476111	AA476111 Sequence
3	14.8	59.12	25	6	AA476112	AA476112 Sequence
4	14.8	59.12	25	6	AA476113	AA476113 Sequence
5	14.8	59.12	25	6	AA476114	AA476114 Sequence
6	14.8	59.12	25	6	AA476115	AA476115 Sequence
7	14.8	59.12	25	6	AA476116	AA476116 Sequence
8	14.8	59.12	25	6	AA476117	AA476117 Sequence
9	14.8	59.12	25	6	AA476118	AA476118 Sequence
10	14.6	58.4	28	6	AA13117	AA13117 Sequence
11	14.4	57.6	31	6	AA6421	AA6421 Sequence
12	14.4	57.6	31	6	AA6422	AA6422 Sequence
13	14.2	56.8	31	6	AA4361	AA4361 Sequence
14	14.2	56.8	29	6	AA152172	AA152172 Sequence
15	14.2	56.8	29	6	AA6426	AA6426 Sequence
16	14.2	56.8	31	6	AA48661	AA48661 Sequence
17	14	56.0	27	22	BD042094	BD042094 Human SGI
18	14	56.0	27	22	BD042574	BD042574 Human SGI
19	14	56.0	27	22	AA120116	AA120116 Sequence
20	14	56.0	30	6	AA6016	AA6016 Sequence
21	13.8	55.12	17	6	AA475123	AA475123 Sequence
22	13.8	55.12	17	6	AA475124	AA475124 Sequence
23	13.8	55.12	20	6	AA179914	AA179914 Sequence
24	13.8	55.12	25	6	AA043229	AA043229 Sequence
25	13.8	55.12	25	6	AA475512	AA475512 Sequence
26	13.6	54.4	25	6	AA475119	AA475119 Sequence
27	13.6	54.4	22	6	AA60176	AA60176 Sequence
28	13.6	54.4	24	6	AA6476	AA6476 Sequence
29	13.6	54.4	25	6	AA425795	AA425795 Sequence
30	13.6	54.4	25	6	AA425796	AA425796 Sequence
31	13.6	54.4	25	6	AA004316	AA004316 Sequence
32	13.6	54.4	30	6	AA004741	AA004741 Sequence
33	13.6	54.4	30	6	AA008827	AA008827 Sequence
34	13.6	54.4	30	6	AA008827	AA008827 Sequence
35	13.6	54.4	30	6	AA137011	AA137011 Sequence
36	13.6	54.4	30	6	171011	171011 Sequence
37	13.6	54.4	30	6	181006	181006 Sequence
38	13.6	54.4	30	6	181102	181102 Sequence
39	13.4	53.6	31	6	AA079777	AA079777 Sequence
40	13.4	53.6	31	6	AA081907	AA081907 Sequence
41	13.4	53.6	31	6	AA170667	AA170667 Sequence
42	13.4	53.6	31	6	AA424856	AA424856 Sequence
43	13.2	52.8	19	6	AA119926	AA119926 Sequence
44	13.2	52.8	27	6	AA125178	AA125178 Sequence
45	13.2	52.8	27	6	AA125179	AA125179 Sequence
46	13.2	52.8	30	6	AA425192	AA425192 Sequence
47	13	52.0	30	6	AA146669	AA146669 Sequence
48	13	52.0	25	6	AA044334	AA044334 Sequence
49	13	52.0	25	6	AA133117	AA133117 Sequence
50	13	52.0	25	6	EA9950	EA9950 Sequence
51	13	52.0	29	6	186015	186015 Sequence
52	13	52.0	29	6	AA115794	AA115794 Sequence
53	13	52.0	30	6	186014	186014 Sequence
54	13	52.0	31	6	AA077933	AA077933 Sequence
55	13	52.0	31	6	186341	186341 Sequence
56	13	52.0	31	6	AA475130	AA475130 Sequence
57	12.8	51.12	20	6	AA119947	AA119947 Sequence
58	12.8	51.12	21	6	AA6467	AA6467 Sequence
59	12.8	51.12	21	6	AA050995	AA050995 Sequence
60	12.8	51.12	24	6	AA454835	AA454835 Sequence
61	12.8	51.12	25	6	AA411257	AA411257 Sequence
62	12.8	51.12	25	6	AA411257	AA411257 Sequence
63	12.8	51.12	25	6	AA044346	AA044346 Sequence
64	12.8	51.12	25	6	AA044346	AA044346 Sequence
65	12.8	51.12	25	6	AA044346	AA044346 Sequence



## ORGANISM

Mus musculus

## REFERENCE

Eukaryota; Metazoa; Chordata; Gnathata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 27)

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmood,M., Meenen,F., Pedersen,T., Pelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

## TITLE

Mouse whole-genome scaffolding with paired end reads from 10kb

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Box 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0080 Row: 0 Column: 08

Seq primer: CTTGTAAATCACTGACGTCAGT

Class: plasmid ends

High quality sequence stop: 27.

Location/Qualifiers

## FEATURES

1..27

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="MUGC2M090008"

/clone\_lib="Mouse 10kb plasmid mUGM library"

/sex="Male"

/lab\_host="F. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD42uv. Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g[472114]g[AF199221]), a copy number

inducible derivative of plasmid p1. The vector was ligated

with adaptor complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent F. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

## BASE COUNT

12 a 6 c 8 g 1 t

## ORIGIN

## Query Match

42.48; Score 10.6; DB 17; Length 27;

Best local similarity 76.58; Pred. No. 9.7e+05;

Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

## QY

6 GAGCCGAGAAAGATGAG 22

## Zh

3 GAGCCGAGAAAGATGAG 19

Search completed: July 21, 2003, 15:48:14  
Job time : 665.467 secs





[illegible][illegible]

0.005 inch efficiency. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 2.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD19 (31473214) (AF103722.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adapters complementary to the insert adapters and purified. The sheared, adaptered mouse DNA was annealed to adaptered vector DNA and transformed into chemically-competent *Escherichia coli* (Stratagene) cells and selected for ampicillin resistance.

Query Match 43.2% Score 10.8; DB 17; Length 32;  
Best Local Similarity 85.7% Pred No. 8.3e+05;  
Matches 12, Conservative 0, Mismatches 2, Indels 0, Gaps 0

QY 10 CCAAGACATGAG 23  
|||||  
28 CCAAGACATGAG 15

RESULT 31  
A0358679 23 bp mRNA (blast EST 28 APR 2003)  
Accession BED0003469 3', mRNA sequence.  
Version A0358679.1 GI:20924472  
Keywords house mouse  
Source Mus musculus  
Organism Mus musculus

REFERENCE  
AUTHORS Kato, K. and Matoba, R.  
TITLE Generation of expressed sequence tags from mouse brain  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kikuya Kato  
Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
Tel: 81-743-72-5581  
Fax: 81-743-72-5580  
Email: kkat@is.nara.ac.jp,  
http://www2.is.nara.ac.jp/REF/index.html

FEATURES  
SOURCE 1..33  
Location/Qualifiers  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="BED003469"  
/tissue="brain"  
/note="Vector: pCMV-Tagsy"

BASE COUNT 16 a 5 c 7 g 5 t  
ORIGIN  
Query Match 43.2% Score 10.8; DB 17; Length 32;  
Best Local Similarity 85.7% Pred No. 8.3e+05;  
Matches 12, Conservative 0, Mismatches 2, Indels 0, Gaps 0

QY 10 CCAAGACATGAG 23  
|||||  
28 CCAAGACATGAG 15

RESULT 32  
A0358679 33 bp mRNA (blast EST 28 APR 2003)  
Accession A0358679.1 GI:20924472

DEFINITION A0358679.1 directed mouse cDNA library Mus musculus cDNA clone  
BED003469 3', mRNA sequence.  
ACCESSION BED003469  
VERSION A0358679.1 GI:20924472  
KEYWORDS EST

SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Kato, K. and Matoba, R.  
TITLE Generation of expressed sequence tags from mouse brain  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kikuya Kato  
Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
Tel: 81-743-72-5581  
Fax: 81-743-72-5580  
Email: kkat@is.nara.ac.jp,  
http://www2.is.nara.ac.jp/REF/index.html

FEATURES  
SOURCE 1..33  
Location/Qualifiers  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="BED003469"  
/tissue="brain"  
/note="Vector: pCMV-Tagsy"

BASE COUNT 16 a 5 c 7 g 5 t  
ORIGIN  
Query Match 43.2% Score 10.8; DB 17; Length 32;  
Best Local Similarity 85.7% Pred No. 8.3e+05;  
Matches 12, Conservative 0, Mismatches 2, Indels 0, Gaps 0

QY 10 CCAAGACATGAG 23  
|||||  
28 CCAAGACATGAG 15

RESULT 33  
A032495 34 bp mRNA (blast EST 28 APR 2003)  
Accession A032495.1 GI:1951621  
Version A032495.1  
Keywords human.  
Source Homo sapiens  
Organism Homo sapiens

REFERENCE  
AUTHORS Eukaryotic Melendez-Chavez, C. and Matoba, R.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP)  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgap@is.nara.ac.jp  
This clone is available through the  
IMAGE Consortium (info@img.org) for further information.  
Insert Length: 1624  
Seq primer: 40m3 fwd, RT from Amsterdam  
High quality sequence stop: 1.

FEATURES  
SOURCE 1..34  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1654738"  
/tissue="brain"

ORIGIN  
Query Match 43.2% Score 10.8; DB 17; Length 32;  
Best Local Similarity 85.7% Pred No. 8.3e+05;  
Matches 12, Conservative 0, Mismatches 2, Indels 0, Gaps 0



```

ORGANISM      Human.
SOURCE        Homo sapiens.
REFERENCE     Partridge, M., 1993, Chetani, C., 1993, Vardi, A., Estabrooke,
Mammalia: Primates: Catarrhini: Hominoidea, Hominidae, Hominini
1 (bases 1 to 31)
REFERENCE     NCBI-CCAT http://www.ncbi.nlm.nih.gov/ccat.asp.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JCENTRAL      Tumor Gene Index
COMMENT        Registered: 11/97
JCENTRAL      Contact: Robert Strassberg, Ph.D.
Email: cgap@remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Matti, M.D.
CDNA Library Preparation: M. Bustin, Charles, Ph.D., M. Fatima
Honnold, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Cloned distribution: NCIC-CCAT clone distribution information can be
found through the I.M.A.G.E. Consortium/BLAST at:
www.bio.1111.gw/hcf/image/image.html

FEATURES
SOURCE
1
11
Location/Qualifiers
1..31
/organism="Homo sapiens"
/db="refseq"
/clone="IMAGE:1298158"
/clone_lib="NCI-CCAT-CTRI"
/tissue_type="germinal center B cell"
/lab_host="MDH10B"
rev="reverse"
cdna="cDNA"
polymer="poly(A)"
Note: Strong Eco RI, Not I, and Pst I sites were
was restriction from human testis with the following:
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NHLI), Dr. David Allman
(NCI) and Dr. Gerald Matti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-GTTTACCATTTTAAAGGAGATGATGAGT-3'
15'-Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pGTT vector library
went through the kind of characterization, and was
"confirmed by PCR" (Chen and M. Fatima Honnold)."
a
11
8
21

Query Match 43.2% Score: 16.4; E-9; Length: 31;
Best Local Similarity: 68.2%, Field No. 9,260,977;
Matches: 11, Conservative: 7, Indels: 0, Gaps: 0.

4 CTGAGGCGTAAAGATGATGAGT 25
|||||  |||  |||  |||
3 CTGAGGCGTAAAGATGATGAGT 24

RESULT 27
LOCUS       A1143422
DEFINITION  Homo sapiens cDNA clone IMAGE 1430633
3' similar to CTGAGGCGTAAAGATGATGAGT (IMAGE 1430633)
sequence.
A1143422
A1143422 1 31 3667011
EST.
human.
Homo sapiens
Pituitary, Anterior, Chetani, C., 1993, Vardi, A., Estabrooke,
Mammalia: Primates: Catarrhini: Hominoidea, Hominidae, Hominini
1 (bases 1 to 31)
REFERENCE     NCBI-CCAT http://www.ncbi.nlm.nih.gov/ccat.asp.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JCENTRAL      Tumor Gene Index
COMMENT        Registered: 11/97
JCENTRAL      Contact: Robert Strassberg, Ph.D.
Email: cgap@remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Matti, M.D.
CDNA Library Preparation: M. Bustin, Charles, Ph.D., M. Fatima
Honnold, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Cloned distribution: NCIC-CCAT clone distribution information can be
found through the I.M.A.G.E. Consortium/BLAST at:
www.bio.1111.gw/hcf/image/image.html

Trace considered overall poor quality
Insert length: 842 Std Error: 0.00
Seq primer: 40m13 fwd pr from Amplicam
High quality sequence steps: 1
Location/Qualifiers
1
11
/organism="Homo sapiens"
/db="refseq"
/clone="IMAGE:1298158"
/clone_lib="NCI-CCAT-CTRI"
/tissue_type="germinal center B cell"
/lab_host="MDH10B"
rev="reverse"
cdna="cDNA"
polymer="poly(A)"
Note: Strong Eco RI, Not I, and Pst I sites were
was restriction from human testis with the following:
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NHLI), Dr. David Allman
(NCI) and Dr. Gerald Matti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-GTTTACCATTTTAAAGGAGATGATGAGT-3'
15'-Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pGTT vector library
went through the kind of characterization, and was
"confirmed by PCR" (Chen and M. Fatima Honnold)."
a
11
8
21

```

FEATURES	Source	Location/Qualifiers
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (NCI)	
TUMOR	Tumor Gene Index	
COMMENT	NCI-60 Cell Line, Ph.D.	
EMAIL	Email: cga@nci.nih.gov	
TRACE	This data is available legally free through NCI. For further information, please contact the NCI Information Center (info@nci.nih.gov).	
TRACE	Trace considered overall poor quality	
Seq	Seq primer: 40013 fwd R from Amersham	
High	High quality sequence strip: 1.	
Location	Location/Qualifiers	
1. 31		
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/clone="IMAGE:1690639"		
/clone_lib="Scatter NHPNP St"		
/isolate="F1" "F2" "F3" "F4" "F5" "F6" "F7" "F8" "F9" "F10" "F11" "F12" "F13" "F14" "F15" "F16" "F17" "F18" "F19" "F20" "F21" "F22" "F23" "F24" "F25" "F26" "F27" "F28" "F29" "F30" "F31" "F32" "F33" "F34" "F35" "F36" "F37" "F38" "F39" "F40" "F41" "F42" "F43" "F44" "F45" "F46" "F47" "F48" "F49" "F50" "F51" "F52" "F53" "F54" "F55" "F56" "F57" "F58" "F59" "F60" "F61" "F62" "F63" "F64" "F65" "F66" "F67" "F68" "F69" "F70" "F71" "F72" "F73" "F74" "F75" "F76" "F77" "F78" "F79" "F80" "F81" "F82" "F83" "F84" "F85" "F86" "F87" "F88" "F89" "F90" "F91" "F92" "F93" "F94" "F95" "F96" "F97" "F98" "F99" "F100" "F101" "F102" "F103" "F104" "F105" "F106" "F107" "F108" "F109" "F110" "F111" "F112" "F113" "F114" "F115" "F116" "F117" "F118" "F119" "F120" "F121" "F122" "F123" "F124" "F125" "F126" "F127" "F128" "F129" "F130" "F131" "F132" "F133" "F134" "F135" "F136" "F137" "F138" "F139" "F140" "F141" "F142" "F143" "F144" "F145" "F146" "F147" "F148" "F149" "F150" "F151" "F152" "F153" "F154" "F155" "F156" "F157" "F158" "F159" "F160" "F161" "F162" "F163" "F164" "F165" "F166" "F167" "F168" "F169" "F170" "F171" "F172" "F173" "F174" "F175" "F176" "F177" "F178" "F179" "F180" "F181" "F182" "F183" "F184" "F185" "F186" "F187" "F188" "F189" "F190" "F191" "F192" "F193" "F194" "F195" "F196" "F197" "F198" "F199" "F200" "F201" "F202" "F203" "F204" "F205" "F206" "F207" "F208" "F209" "F210" "F211" "F212" "F213" "F214" "F215" "F216" "F217" "F218" "F219" "F220" "F221" "F222" "F223" "F224" "F225" "F226" "F227" "F228" "F229" "F230" "F231" "F232" "F233" "F234" "F235" "F236" "F237" "F238" "F239" "F240" "F241" "F242" "F243" "F244" "F245" "F246" "F247" "F248" "F249" "F250" "F251" "F252" "F253" "F254" "F255" "F256" "F257" "F258" "F259" "F260" "F261" "F262" "F263" "F264" "F265" "F266" "F267" "F268" "F269" "F270" "F271" "F272" "F273" "F274" "F275" "F276" "F277" "F278" "F279" "F280" "F281" "F282" "F283" "F284" "F285" "F286" "F287" "F288" "F289" "F290" "F291" "F292" "F293" "F294" "F295" "F296" "F297" "F298" "F299" "F300" "F301" "F302" "F303" "F304" "F305" "F306" "F307" "F308" "F309" "F310" "F311" "F312" "F313" "F314" "F315" "F316" "F317" "F318" "F319" "F320" "F321" "F322" "F323" "F324" "F325" "F326" "F327" "F328" "F329" "F330" "F331" "F332" "F333" "F334" "F335" "F336" "F337" "F338" "F339" "F340" "F341" "F342" "F343" "F344" "F345" "F346" "F347" "F348" "F349" "F350" "F351" "F352" "F353" "F354" "F355" "F356" "F357" "F358" "F359" "F360" "F361" "F362" "F363" "F364" "F365" "F366" "F367" "F368" "F369" "F370" "F371" "F372" "F373" "F374" "F375" "F376" "F377" "F378" "F379" "F380" "F381" "F382" "F383" "F384" "F385" "F386" "F387" "F388" "F389" "F390" "F391" "F392" "F393" "F394" "F395" "F396" "F397" "F398" "F399" "F400" "F401" "F402" "F403" "F404" "F405" "F406" "F407" "F408" "F409" "F410" "F411" "F412" "F413" "F414" "F415" "F416" "F417" "F418" "F419" "F420" "F421" "F422" "F423" "F424" "F425" "F426" "F427" "F428" "F429" "F430" "F431" "F432" "F433" "F434" "F435" "F436" "F437" "F438" "F439" "F440" "F441" "F442" "F443" "F444" "F445" "F446" "F447" "F448" "F449" "F450" "F451" "F452" "F453" "F454" "F455" "F456" "F457" "F458" "F459" "F460" "F461" "F462" "F463" "F464" "F465" "F466" "F467" "F468" "F469" "F470" "F471" "F472" "F473" "F474" "F475" "F476" "F477" "F478" "F479" "F480" "F481" "F482" "F483" "F484" "F485" "F486" "F487" "F488" "F489" "F490" "F491" "F492" "F493" "F494" "F495" "F496" "F497" "F498" "F499" "F500" "F501" "F502" "F503" "F504" "F505" "F506" "F507" "F508" "F509" "F510" "F511" "F512" "F513" "F514" "F515" "F516" "F517" "F518" "F519" "F520" "F521" "F522" "F523" "F524" "F525" "F526" "F527" "F528" "F529" "F530" "F531" "F532" "F533" "F534" "F535" "F536" "F537" "F538" "F539" "F540" "F541" "F542" "F543" "F544" "F545" "F546" "F547" "F548" "F549" "F550" "F551" "F552" "F553" "F554" "F555" "F556" "F557" "F558" "F559" "F560" "F561" "F562" "F563" "F564" "F565" "F566" "F567" "F568" "F569" "F570" "F571" "F572" "F573" "F574" "F575" "F576" "F577" "F578" "F579" "F580" "F581" "F582" "F583" "F584" "F585" "F586" "F587" "F588" "F589" "F590" "F591" "F592" "F593" "F594" "F595" "F596" "F597" "F598" "F599" "F600" "F601" "F602" "F603" "F604" "F605" "F606" "F607" "F608" "F609" "F610" "F611" "F612" "F613		





musculus cecp1.67 (718) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrolytically sheared by repeated passage through a 0.006 inch nitrocellulose velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2.3(314703143p/AP1000) by a copy-number inducible derivative of plasmid p1. The vector was ligated with adapters complementary to the insert adapters and purified. The sheared, adaptered mouse DNA was annealed to adaptered vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 9 c 12 g 9 t  
ORIGIN  
Query Match 44.08% Score 117 DB 177 Length 331  
Best Local Similarity 100%, Prod No. 7.6e+09  
Matches 117 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 4 GTCCAGCCGCGAA 14  
|||||  
Db 22 CCGAGCCGCGAA 12

RESULT 22  
AZ821732 26 bp DNA Linear GSS 16 FEB 2001  
LOCUS 2609461p Mouse 109b plasmid library mouse musculus generic  
DEFINITION clone U06770094p17 R, DNA sequence.  
ACCESSION AZ821732  
VERSION AZ821732.1 GI:12391640  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota, Mammalia, Chordata, Euteleostomi, Euteleostomi, Mammalia, Euteleostomi, Rodentia, Saurimorphi, Muridae, Muridae, Mus (bases 1 to 26)  
Curtis, A. J. A., Butler, M., Edwards, T., Dwyer, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Menden, E., Pedersen, T., Reilly, M., Rose, M., Rose, P., Stoeck, P., Tilly, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 109b plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert R. Weiss  
University of Utah Genome Center  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunnagen@utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plates: 0027 Row: 6 Column: 17  
Seq primer: CACACAGAAACAGATATACAC  
Class: plasmid ends  
High quality sequence step: 21  
Location/Qualifiers  
1..26

FEATURES  
SOURCE  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06770094p17"  
/date="17 Feb 2001"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, TransFormant, F"  
/note="Vector: pMD2.3(314703143p/AP1000) plasmid DNA from M.

musculus cecp1.67 (718) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrolytically sheared by repeated passage through a 0.006 inch nitrocellulose velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2.3(314703143p/AP1000) by a copy-number inducible derivative of plasmid p1. The vector was ligated with adapters complementary to the insert adapters and purified. The sheared, adaptered mouse DNA was annealed to adaptered vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 9 c 3 g 7 t  
ORIGIN  
Query Match 43.24% Score 10.8, DB 177 Length 331  
Best Local Similarity 100%, Prod No. 7.6e+09  
Matches 127 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 GTCCAGCCGCGAA 15  
|||||  
Db 15 GTCCAGCCGCGAA 2

RESULT 23  
AZ821732 26 bp DNA Linear GSS 16 FEB 2001  
LOCUS 2609461p Mouse 109b plasmid library mouse musculus generic  
DEFINITION clone U06770094p17 R, DNA sequence.  
ACCESSION AZ821732  
VERSION AZ821732.1 GI:12391640  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota, Mammalia, Chordata, Euteleostomi, Euteleostomi, Mammalia, Euteleostomi, Rodentia, Saurimorphi, Muridae, Muridae, Mus (bases 1 to 26)  
Curtis, A. J. A., Butler, M., Edwards, T., Dwyer, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Menden, E., Pedersen, T., Reilly, M., Rose, M., Rose, P., Stoeck, P., Tilly, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 109b plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert R. Weiss  
University of Utah Genome Center  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunnagen@utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plates: 0027 Row: 6 Column: 17  
Seq primer: CACACAGAAACAGATATACAC  
Class: plasmid ends  
High quality sequence step: 26  
Location/Qualifiers  
1..26

FEATURES  
SOURCE  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06770094p17"  
/date="17 Feb 2001"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, TransFormant, F"  
/note="Vector: pMD2.3(314703143p/AP1000) plasmid DNA from M.

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/note="Vector: PMD42nv; Purified genomic DNA:

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Email: dunnugenetics.utah.edu  
 Insert Length: 1000 bp Error: 0.00  
 Plates: 0165 Low: 2 Column: 15  
 Seq primer: CACACAGCAACACATATGACG  
 Class: Plasmid ends  
 High quality sequence stop: 27

## FEATURES

source

1..27  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="MIM155515"  
 /clone\_11b="mouse 10kb plasmid insert library"  
 /sex="Male"  
 /at\_pos="F" Full strain XhoI-SacI, PstI-resistant, P-  
 1.0 kb "XhoI" PstI-SacI, PstI-SacI, PstI-SacI, PstI-SacI  
 Musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/protocols/dnares/). The DNA  
 was high-dynamically screened by region of passage through a  
 0.005 inch efficiency at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adapter oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapter DNA was purified and size selected for a 2.5 to  
 10 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD19 (GibcoBRL) (pMD19-1), a copy number  
 inducible derivative of plasmid p1. The vector was ligated  
 with adapters complementary to the insert adapters and  
 purified. The sheared, adapter mouse DNA was introduced to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XhoI-SacI (Stratagene) cells  
 and selected for ampicillin resistance."

## BASE COUNT

ORIGIN  
 a 4 0% Score 11: 28 17: Length 27:  
 5 c 11 g 3 t

Query Match 44.0% Score 11: 28 17: Length 27:  
 Best Local Similarity 73.3% Fied Res. 6.6e-05  
 Matches 14: Conservative 0: Mismatches 5: Gaps 0:

4 30GAGGCGGAAATGATG 21  
 4 CAGGCGGAAATGATG 22

RESULT 18  
 A2817062/7  
 LOCUS 28 bp DNA linear GEN 20 FEB 2001  
 DEFINITION Mouse 10kb plasmid insert library Mus musculus genomic  
 clone U99000000.1, F, DNA sequence.  
 ACCESSION A2817062  
 VERSION A2817062.1 GI:12966070  
 GSS  
 SOURCE house mouse  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Euteleostomi; Eumetazoa; Mammalia;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Murinae; Mus;  
 1 (bases 1 to 28)

## REFERENCE

AUTHORS Dunn, D., Ayayla, A., Parker, M., Pearson, T., Dival, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Weigh, E., Pedersen, T., Kelly,  
 M., Rose, M., Rose, P., Stokes, P., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse 10kb genomic clone library with failed and reads from 10kb  
 plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)  
 CONTACT: Robert E. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Pm. 104, Rm. 1111 Flynn's Power Bldg., 203 203 E. 500, UT  
 4412, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: dunnugenetics.utah.edu  
 Insert Length: 1000 bp Error: 0.00  
 Plates: 0086 Low: A Column: 12  
 Seq primer: CATTGTAACAGACAGGCAAT  
 Class: Plasmid ends  
 High quality sequence stop: 30.

## FEATURES

source

1..30  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="MIM255512"  
 /clone\_11b="mouse 10kb plasmid insert library"  
 /sex="Male"  
 /at\_pos="F" Full strain XhoI-SacI, PstI-resistant, P-  
 1.0 kb "XhoI" PstI-SacI, PstI-SacI, PstI-SacI, PstI-SacI  
 Musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/protocols/dnares/). The DNA  
 was high-dynamically screened by region of passage through a  
 0.005 inch efficiency at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adapter oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapter DNA was purified and size selected for a 2.5 to  
 10 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD19 (GibcoBRL) (pMD19-1), a copy number  
 inducible derivative of plasmid p1. The vector was ligated  
 with adapters complementary to the insert adapters and  
 purified. The sheared, adapter mouse DNA was introduced to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XhoI-SacI (Stratagene) cells  
 and selected for ampicillin resistance."

## BASE COUNT

ORIGIN  
 a 4 0% Score 11: 28 17: Length 30:  
 5 c 11 g 3 t

Query Match 44.0% Score 11: 28 17: Length 30:  
 Best Local Similarity 73.3% Fied Res. 6.6e-05  
 Matches 14: Conservative 0: Mismatches 5: Gaps 0:

4 30GAGGCGGAAATGATG 21  
 26 TCTCAGCTTAAAGAGGGA 8

RESULT 19  
 BH789954/5  
 LOCUS 28 bp DNA linear GEN 20 FEB 2001  
 DEFINITION Mouse 10kb plasmid insert library Mus musculus genomic  
 clone U99000000.1, F, DNA sequence.  
 ACCESSION BH789954  
 VERSION BH789954.1 GI:1994052  
 GSS  
 SOURCE house mouse  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Euteleostomi; Eumetazoa; Mammalia;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Murinae; Mus;  
 1 (bases 1 to 28)

## REFERENCE

AUTHORS Dunn, D., Ayayla, A., Parker, M., Pearson, T., Dival, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Weigh, E., Pedersen, T., Kelly,  
 M., Rose, M., Rose, P., Stokes, P., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.  
 Mouse 10kb genomic clone library with failed and reads from 10kb  
 plasmid inserts

## JOURNAL

COMMENT Unpublished (2001)  
 CONTACT: Joseph P. Ecker  
 Salk Institute Genomic Analysis Laboratory (GAL) 10550  
 The Salk Institute for Biological Studies  
 10550 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379







```

/Ab_vif-"Avon-10000"
/Colony="MMP2-Mouse81604"
/ColonyLib="Mouse 10k plasmid TIGR library"
/sex="Male"
/lab host="E. Coli strain XL10-gold, TI-resistant, F-"
"/lab host="T. pyrrocy, Puffin-l gene, DNA from W. muscivora (GFRU/SC) male" was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Appropriate oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD47 (G147314 JEFAP07) using a 231 number inducible derivative of plasmid R1. The vector was ligated with appropriate complementary to the insert adapters and purified. The sheared, adapter-mouse DNA was annealed to adapter vector RNA, and transformed into chemically competent E. coli XL10 Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT
      12 a          6 c          13 g          6 t
ORIGIN
Query Match       46.4% Score 11.6 DB:17 Length 31;
Post local similarity 77.8%; P-val: 1.6e-05;
Matches 141 Conservative 0 Mismatches 4 Indels 0 Gaps 0
Cv
7 AATCCCAAAATCATAGCT 24
  ||| ||||| ||||| ||
  2 AGGAAATTATATTAAGT 19
RESULT 9
TATGACGCG
TATGACGCG/C
LUNTS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
CONSTRUCTED AT THE INSTITUTE FOR GENOME RESEARCH (TIGR), ROCKVILLE, MD. MOUSE TNA ISOLATED FROM A CLONED POPULATION OF TYMPANOMA LUNG EPITHELIAL CELLS (10.1) WAS MECHANICALLY SHEARED TO GIVE A LIGHT SIZE DISTRIBUTION (4 kb). THE VECT METHOD USED FOR THE LIBRARY CONSTRUCTION IS DESCRIBED IN DETAIL IN SMITH, H., AND VENTER, J.C. MAKING SMALL INSERT LIBRARIES FOR WHOLE GENOME SHOTGUN SEQUENCING PROJECTS. IN Genome Sequencing: A Practical Approach, eds M. Vaubin and R. Barrell, Oxford University Press, 1999. Email: mols@vc.tigr.edu. Details of T. bruneri sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Tig/JEFAP07/index.html. Location/Qualifiers
1..24
organism="Tympnosoma Brucei"
strain="TEB0927"

```

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/tp xrf="taxon:5691"
/clone="78c03"
43 69 114 1917 Length 24
Best local similarity 71.4% Pred No. 4,1e+05;
Matches 15, Conservative 0, Mismatches 6, Indels 0, Gaps 0
2 GTGATATTCACAAATATGAC 22
|||||
21 GTATATATACAAATATGAC 1

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Query Match 43 69 114 1917 Length 24  
 Best local similarity 71.4% Pred No. 4,1e+05;  
 Matches 15, Conservative 0, Mismatches 6, Indels 0, Gaps 0

RESULT 10  
 LOCUS AA920864  
 DEFINITION  
 ACCESSION AA920864  
 VERSION AA920864.1 GI:1097643  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 REFERENCE Bukaryota; Melarzo; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sauriophata; Muridae; Murinae; Mus.  
 1 (bases 1 to 31)  
 Maita, M., Hillier, D., Allen, M., Bowles, M., Dietrich, N., Doherty, T.,  
 Gaitan, S., Hawley, T., Levy, M., Li, W., Martin, G., Morris, M.,  
 Schellander, K., Stephens, M., Tan, F., Underwood, P., Moore, B.,  
 Theising, P., Wylie, T., Leunich, G., Soares, R., Wilson, R., and  
 Maleson, R.  
 The WashU-HMI Mouse EST Project  
 Unpublished (1996)  
 CONTACT: Maria M. Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8001, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through DDBJ. Contact the  
 IMAGE Consortium (info@imga.jnl.gov) for further information.  
 MGI:683172  
 Trace Subtracted overall poor quality  
 Possible reversed strand similarity to cDNA  
 Seq primer: 28m3 rev: RT from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
 /clone="IMAGE:112876"  
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 /tissue="type:"macrophage"  
 /dev\_stage="WEHI-3 cell line"  
 /lab\_host="scf" "antigen resistant"  
 /notes="scf host, cloned from WEHI-3 cell line, cloned unidirectionally. Primer:  
 Oligo dT, WEHI-3 cell line. Average insert size 1.5 kb.  
 3'-5' adaptor sequence: 5' GTATGATATTCACAAATATGAC 3' "

BASE COUNT 11 a 3 6 c 12 g  
 ORIGIN  
 43 69 114 1917 Length 24  
 Best local similarity 71.4% Pred No. 4,1e+05;  
 Matches 15, Conservative 0, Mismatches 6, Indels 0, Gaps 0

4 CCAGAGCCAGAAAGATGACT 24  
 6 CGAGAGAGAGAAACAGAGACT 26

City Water 47 84 9430 112 5P 112 10000000  
Best Local Similarity 99 84 9430 112 5P 112 10000000  
Number of Connections 100 9430 112 5P 112 10000000

[illegible]

```

RESULT 8
AZ815323
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHOR
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE
1.31
/organism="Mus musculus"
/strain="C57BL/60"

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[illegible]

[illegible]

[illegible]





80	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	153	9.6	39.4	29.4	29	17	EH449479
81	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	154	9.6	39.4	29.4	29	17	EH449479
82	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	155	9.6	39.4	29.4	29	17	EH449479
83	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	156	9.6	39.4	29.4	29	17	EH449479
84	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	157	9.6	39.4	29.4	29	17	EH449479
85	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	158	9.6	39.4	29.4	29	17	EH449479
86	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	159	9.6	39.4	29.4	29	17	EH449479
87	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	160	9.6	39.4	29.4	29	17	EH449479
88	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	161	9.6	39.4	29.4	29	17	EH449479
89	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	162	9.6	39.4	29.4	29	17	EH449479
90	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	163	9.6	39.4	29.4	29	17	EH449479
91	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	164	9.6	39.4	29.4	29	17	EH449479
92	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	165	9.6	39.4	29.4	29	17	EH449479
93	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	166	9.6	39.4	29.4	29	17	EH449479
94	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	167	9.6	39.4	29.4	29	17	EH449479
95	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	168	9.6	39.4	29.4	29	17	EH449479
96	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	169	9.6	39.4	29.4	29	17	EH449479
97	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	170	9.6	39.4	29.4	29	17	EH449479
98	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	171	9.6	39.4	29.4	29	17	EH449479
99	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	172	9.6	39.4	29.4	29	17	EH449479
100	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	173	9.6	39.4	29.4	29	17	EH449479
101	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	174	9.6	39.4	29.4	29	17	EH449479
102	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	175	9.6	39.4	29.4	29	17	EH449479
103	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	176	9.6	39.4	29.4	29	17	EH449479
104	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	177	9.6	39.4	29.4	29	17	EH449479
105	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	178	9.6	39.4	29.4	29	17	EH449479
106	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	179	9.6	39.4	29.4	29	17	EH449479
107	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	180	9.6	39.4	29.4	29	17	EH449479
108	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	181	9.6	39.4	29.4	29	17	EH449479
109	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	182	9.6	39.4	29.4	29	17	EH449479
110	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	183	9.6	39.4	29.4	29	17	EH449479
111	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	184	9.6	39.4	29.4	29	17	EH449479
112	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	185	9.6	39.4	29.4	29	17	EH449479
113	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	186	9.6	39.4	29.4	29	17	EH449479
114	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	187	9.6	39.4	29.4	29	17	EH449479
115	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	188	9.6	39.4	29.4	29	17	EH449479
116	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	189	9.6	39.4	29.4	29	17	EH449479
117	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	190	9.6	39.4	29.4	29	17	EH449479
118	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	191	9.6	39.4	29.4	29	17	EH449479
119	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	192	9.6	39.4	29.4	29	17	EH449479
120	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	193	9.6	39.4	29.4	29	17	EH449479
121	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	194	9.6	39.4	29.4	29	17	EH449479
122	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	195	9.6	39.4	29.4	29	17	EH449479
123	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	196	9.6	39.4	29.4	29	17	EH449479
124	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	197	9.6	39.4	29.4	29	17	EH449479
125	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	198	9.6	39.4	29.4	29	17	EH449479
126	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	199	9.6	39.4	29.4	29	17	EH449479
127	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	200	9.6	39.4	29.4	29	17	EH449479
128	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	201	9.6	39.4	29.4	29	17	EH449479
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130	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	203	9.6	39.4	29.4	29	17	EH449479
131	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	204	9.6	39.4	29.4	29	17	EH449479
132	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	205	9.6	39.4	29.4	29	17	EH449479
133	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	206	9.6	39.4	29.4	29	17	EH449479
134	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	207	9.6	39.4	29.4	29	17	EH449479
135	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	208	9.6	39.4	29.4	29	17	EH449479
136	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	209	9.6	39.4	29.4	29	17	EH449479
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138	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	211	9.6	39.4	29.4	29	17	EH449479
139	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	212	9.6	39.4	29.4	29	17	EH449479
140	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	213	9.6	39.4	29.4	29	17	EH449479
141	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	214	9.6	39.4	29.4	29	17	EH449479
142	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	215	9.6	39.4	29.4	29	17	EH449479
143	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	216	9.6	39.4	29.4	29	17	EH449479
144	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	217	9.6	39.4	29.4	29	17	EH449479
145	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	218	9.6	39.4	29.4	29	17	EH449479
146	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	219	9.6	39.4	29.4	29	17	EH449479
147	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	220	9.6	39.4	29.4	29	17	EH449479
148	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	221	9.6	39.4	29.4	29	17	EH449479
149	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	222	9.6	39.4	29.4	29	17	EH449479
150	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	223	9.6	39.4	29.4	29	17	EH449479
151	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	224	9.6	39.4	29.4	29	17	EH449479
152	10.2	40.6	34	10	AAV4712	AAV4712	IMC46012	225	9.6	39.4	29.4	29	17	EH449479



2b 24 CCGTGGAGCCGCAAGATGAGT 1

RESULT 38  
US-09-771-933 8

Sequence 8, Application US/09/771-933  
Publication No. US20010092996A1  
GENERAL INFORMATION:  
APPLICANT: Gill-Garrison, Rosalynn E  
APPLICANT: Martin, Christopher J  
APPLICANT: Sanchez Felix, Manuel V  
TITLE OF INVENTION: Computer assisted means for Assessing Lifestyle Risk  
FILE REFERENCE: 620-119  
CURRENT APPLICATION NUMBER: US/09/771-933  
CURRENT FILING DATE: 2001-02-21  
NUMBER OF SEQ ID NOS: 205  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 8  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
US-09-771-933 8

Query Match 51.2%, Score 12.8, DB 15, Length 25,  
Best Local Similarity 78.8%, Pred. No. 1.2e+04,  
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

QY 1 CCGTGGAGCCGCAAGATGAGT 24  
2 CCGTGGAGCCGCAAGATGAGT 25

RESULT 39  
US-10-081-119-11/c

Sequence 11, Application US/10081119  
Publication No. US20030045491A1  
GENERAL INFORMATION:  
APPLICANT: Reinhard, Christoph  
APPLICANT: Jefferson, Anne B.  
APPLICANT: Chan, Vivien W.  
TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic  
FILE REFERENCE: 16932.002  
CURRENT APPLICATION NUMBER: US/10/081-119  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/289,813  
PRIOR FILING DATE: 2001-02-21  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 11  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthesized oligonucleotide  
US-10-081-119-11

Query Match 51.2%, Score 12.8, DB 15, Length 25,  
Best Local Similarity 87.5%, Pred. No. 1.2e+04,  
Matches 14, Conservative 0, Mismatches 2, Indels 0, Gaps 0;

QY 7 AGCCCTAGCAATGAG 22  
17 AGCCCTAGCAATGAG 2

RESULT 40  
US-10-215-112-5162/c

Sequence 5162, Application US/10015112  
Publication No. US20010092996A1  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
TITLE OF INVENTION: Method of Genetic Analysis of Proteins  
FILE REFERENCE: 3119  
CURRENT APPLICATION NUMBER: US/10/215-112  
CURRENT FILING DATE: 2002-08-08  
NUMBER OF SEQ ID NOS: 14916  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 5162  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Cytidine Cytidine Indole  
US-10-215-112-5162

Query Match 51.2%, Score 12.8, DB 15, Length 25,  
Best Local Similarity 78.8%, Pred. No. 1.2e+04,  
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

QY 1 CCGTGGAGCCGCAAGATGAGT 24  
24 CCGTGGAGCCGCAAGATGAGT 1

Search completed: July 23, 2003, 18:30:35  
CPU time: 68.3940 secs





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APPLICATION NUMBER: US/09/303,022
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/05/0,518
FILING DATE: <Unknown>
APPLICATION NUMBER: US/05/944,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/03/945,117
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/00/001,041
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/00/004,100
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/00/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/00/011,561
FILING DATE: 14-APR-1997
APPLICATION NUMBER: US/00/915,607
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/00/974,548
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US/00/974,564
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US/00/974,512
FILING DATE: 01-DEC-1997
APPLICATION NUMBER: US/00/974,500
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 11,052
REFERENCE/AGENT NUMBER: 11,052
TELEPHONE INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: 19-4 Phosphoribosyl-5'-phosphatidyl-
US-09-963-052-40
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
Query Match      53.6%  Score 13.41  DP 113  Length 30
Best Local Similarity 53.6%  Field No. 1341-37
Matches 141  Conservative 0  Mismatches 11  Indels 0  Gaps 0
CY      6  GAGCCGAGAAAGATG 20
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      13  GAGCCGAGAAAGATG 27
Db

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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Patent
US-09-852-990A-1
Query Match      52.3%  Score 13.22  DP 103  Length 24
Best Local Similarity 52.3%  Field No. 7,56+03
Matches 151  Conservative 0  Mismatches 10  Indels 0  Gaps 0
CY      5  GAGCCGAGAAAGATG 22
      ||| ||| ||| |||
      3  GAGCCGAGAAAGATG 20
Db
RESULT 28
US-10-215-112-4405
Sequence 4405, Application US/10015112
Publication No. US2002099296A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
TITLE OF INVENTION: Method of Genetic Analysis of Proteins
FILE REFERENCE: 3119
CURRENT AFFILIATION NUMBER: US/02/015,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4405
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Patent
US-10-215-112-4405
Query Match      52.3%  Score 13.41  DP 159  Length 30
Best Local Similarity 52.3%  Field No. 1341-37
Matches 151  Conservative 0  Mismatches 3  Indels 0  Gaps 0
CY      7  AGGCGAAGAAATTAAGT 24
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      7  AGGCGAAGAAATTAAGT 19
Db
RESULT 29
US-10-215-112-11991
Sequence 11991, Application US/10015112
Publication No. US2002099296A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
TITLE OF INVENTION: Method of Genetic Analysis of Proteins
FILE REFERENCE: 3119
CURRENT AFFILIATION NUMBER: US/02/015,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11991
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Patent
US-10-215-112-11991
Query Match      52.3%  Score 13.41  DP 159  Length 30
Best Local Similarity 52.3%  Field No. 1341-37
Matches 151  Conservative 0  Mismatches 3  Indels 0  Gaps 0
CY      1  GAGCCGAGAAAGATG 18
      ||| ||| ||| |||
      7  GAGCCGAGAAAGATG 24
Db

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1 CURRENT FILING DATE: 2003-01-30
2 PRIOR APPLICATION NUMBER: US/2001-01-30
3 PRIOR FILING DATE: 2001-01-30
4 NUMBER OF SEQ ID NOS: 1
5 SOFTWARE: MEGA 1.0.6
6 SEQ ID NO: 1
7 LENGTH: 25
8 TYPE: DNA
9 ORGANISM: Homo sapiens
10 US-09-866-108-85751

Query Match
Best Local Similarity: 89.28; Score 13.6; DB 10; Length 25;
Matches: 15; Conservation: 6; Mismatches: 1; Indels: 0; Gaps: 0

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
2 25 CACAAAGAAATATATAT 4

RESULT 15
1 Sequence 61, Application US/2001-01-30
2 Publication No. US20020044800A1
3 GENERAL INFORMATION:
4 APPLICANT: Chen, Xuey; Chen, Alex
5 APPLICANT: Yang, Xuey; Min, Theresa J.
6 APPLICANT: Rutankiewicz, Theresa J.
7 TITLE OF INVENTION: IMMUNOMODULATOR E VALINER AND METHOD OF USE THEREOF
8 FILE REFERENCE: IGE-00101.P.1.1
9 CURRENT APPLICATION NUMBER: US/2001-01-30
10 CURRENT FILING DATE: 2002-08-08
11 PRIOR APPLICATION NUMBER: 60/312,120
12 PRIOR FILING DATE: 2001-08-11
13 NUMBER OF SEQ ID NOS: 61
14 SOFTWARE: Patent In Version 3.1
15 SEQ ID NO: 61
16 LENGTH: 30
17 TYPE: DNA
18 ORGANISM: Human (Homo sapiens)
19 US-10-214-524 61

Query Match
Best Local Similarity: 72.03; Score 13.6; DB 10; Length 30;
Matches: 18; Conservation: 0; Mismatches: 1; Indels: 0; Gaps: 0

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
2 28 GGAATGGAATGAAATGATGATG 4

RESULT 16
1 US-09-866-108-11975
2 Sequence 11975, Application US/2001-01-30
3 Patent No. US20020044800A1
4 GENERAL INFORMATION:
5 APPLICANT: GU, Yizhong
6 APPLICANT: JI, Yizhong
7 APPLICANT: HANZHI, David K.
8 APPLICANT: FENG, Shatou G.
9 APPLICANT: FANG, David K.
10 APPLICANT: CHEN, Xuey; Chen, Alex
11 APPLICANT: CHAN, Xuey; Min, Theresa J.
12 TITLE OF INVENTION: METHOD FOR EXPLOITING IN HUMAN HEART AND MYOBLAST
13 FILE REFERENCE: AROMICA-7
14 CURRENT APPLICATION NUMBER: US/2001-01-30
15 CURRENT FILING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: 60/265,475
17 PRIOR FILING DATE: 2000-05-26
18 PRIOR APPLICATION NUMBER: 60/265,475
19 PRIOR FILING DATE: 2000-10-04
20 PRIOR APPLICATION NUMBER: 60/265,475
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1 PRIOR FILING DATE: 2000-01-27
2 PRIOR APPLICATION NUMBER: PCT/US01/00666
3 PRIOR FILING DATE: 2001-01-30
4 PRIOR APPLICATION NUMBER: PCT/US01/00667
5 PRIOR FILING DATE: 2001-01-30
6 PRIOR APPLICATION NUMBER: PCT/US01/00668
7 PRIOR FILING DATE: 2001-01-30
8 PRIOR APPLICATION NUMBER: PCT/US01/00669
9 PRIOR FILING DATE: 2001-01-30
10 PRIOR APPLICATION NUMBER: PCT/US01/00670
11 PRIOR FILING DATE: 2001-01-30
12 PRIOR APPLICATION NUMBER: PCT/US01/00671
13 PRIOR FILING DATE: 2001-01-30
14 PRIOR APPLICATION NUMBER: PCT/US01/00672
15 PRIOR FILING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: PCT/US01/00673
17 PRIOR FILING DATE: 2001-01-30
18 PRIOR APPLICATION NUMBER: PCT/US01/00674
19 PRIOR FILING DATE: 2001-01-30
20 PRIOR APPLICATION NUMBER: PCT/US01/00675
21 PRIOR FILING DATE: 2001-01-30
22 PRIOR APPLICATION NUMBER: PCT/US01/00676
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00677
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: PCT/US01/00678
27 PRIOR FILING DATE: 2001-01-30
28 PRIOR APPLICATION NUMBER: PCT/US01/00679
29 PRIOR FILING DATE: 2001-01-30
30 PRIOR APPLICATION NUMBER: PCT/US01/00680
31 PRIOR FILING DATE: 2001-01-30
32 PRIOR APPLICATION NUMBER: PCT/US01/00681
33 PRIOR FILING DATE: 2001-01-30
34 PRIOR APPLICATION NUMBER: PCT/US01/00682
35 PRIOR FILING DATE: 2001-01-30
36 PRIOR APPLICATION NUMBER: PCT/US01/00683
37 PRIOR FILING DATE: 2001-01-30
38 PRIOR APPLICATION NUMBER: PCT/US01/00684
39 PRIOR FILING DATE: 2001-01-30
40 PRIOR APPLICATION NUMBER: PCT/US01/00685
41 PRIOR FILING DATE: 2001-01-30
42 PRIOR APPLICATION NUMBER: PCT/US01/00686
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44 PRIOR APPLICATION NUMBER: PCT/US01/00687
45 PRIOR FILING DATE: 2001-01-30
46 PRIOR APPLICATION NUMBER: PCT/US01/00688
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52 PRIOR APPLICATION NUMBER: PCT/US01/00691
53 PRIOR FILING DATE: 2001-01-30
54 PRIOR APPLICATION NUMBER: PCT/US01/00692
55 PRIOR FILING DATE: 2001-01-30
56 PRIOR APPLICATION NUMBER: PCT/US01/00693
57 PRIOR FILING DATE: 2001-01-30
58 PRIOR APPLICATION NUMBER: PCT/US01/00694
59 PRIOR FILING DATE: 2001-01-30
60 PRIOR APPLICATION NUMBER: PCT/US01/00695
61 PRIOR FILING DATE: 2001-01-30
62 PRIOR APPLICATION NUMBER: PCT/US01/00696
63 PRIOR FILING DATE: 2001-01-30
64 PRIOR APPLICATION NUMBER: PCT/US01/00697
65 PRIOR FILING DATE: 2001-01-30
66 PRIOR APPLICATION NUMBER: PCT/US01/00698
67 PRIOR FILING DATE: 2001-01-30
68 PRIOR APPLICATION NUMBER: PCT/US01/00699
69 PRIOR FILING DATE: 2001-01-30
70 PRIOR APPLICATION NUMBER: PCT/US01/00700
71 PRIOR FILING DATE: 2001-01-30
72 PRIOR APPLICATION NUMBER: PCT/US01/00701
73 PRIOR FILING DATE: 2001-01-30
74 PRIOR APPLICATION NUMBER: PCT/US01/00702
75 PRIOR FILING DATE: 2001-01-30
76 PRIOR APPLICATION NUMBER: PCT/US01/00703
77 PRIOR FILING DATE: 2001-01-30
78 PRIOR APPLICATION NUMBER: PCT/US01/00704
79 PRIOR FILING DATE: 2001-01-30
80 PRIOR APPLICATION NUMBER: PCT/US01/00705
81 PRIOR FILING DATE: 2001-01-30
82 PRIOR APPLICATION NUMBER: PCT/US01/00706
83 PRIOR FILING DATE: 2001-01-30
84 PRIOR APPLICATION NUMBER: PCT/US01/00707
85 PRIOR FILING DATE: 2001-01-30
86 PRIOR APPLICATION NUMBER: PCT/US01/00708
87 PRIOR FILING DATE: 2001-01-30
88 PRIOR APPLICATION NUMBER: PCT/US01/00709
89 PRIOR FILING DATE: 2001-01-30
90 PRIOR APPLICATION NUMBER: PCT/US01/00710
91 PRIOR FILING DATE: 2001-01-30
92 PRIOR APPLICATION NUMBER: PCT/US01/00711
93 PRIOR FILING DATE: 2001-01-30
94 PRIOR APPLICATION NUMBER: PCT/US01/00712
95 PRIOR FILING DATE: 2001-01-30
96 PRIOR APPLICATION NUMBER: PCT/US01/00713
97 PRIOR FILING DATE: 2001-01-30
98 PRIOR APPLICATION NUMBER: PCT/US01/00714
99 PRIOR FILING DATE: 2001-01-30
100 PRIOR APPLICATION NUMBER: PCT/US01/00715
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US-09-866-108-11980

Query Match: 56.0%, Score 14; DB 10; Length 25;  
 Best Local Similarity: 77.3%, Freq. No. 3,1e+03;  
 Matches: 17; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;

QY 3 TCCGAGCCGAGAGAGATGAGGT 24  
 |||||  
 DB 1 TCCGAGTTATGATGAGAGAGAT 22

RESULT 10  
 US-10-215-112-13122/C

; Sequence 13122, Application US/1009112  
 ; Publication No. US0303233A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Miltman  
 ; TITLE OF INVENTION: Method of Gene Analysis of Polymers  
 ; FILE REFERENCE: 3119  
 ; CURRENT APPLICATION NUMBER: US/10/215,112  
 ; CURRENT FILING DATE: 2002-08-08  
 ; NUMBER OF SEQ. ID NOS: 14936  
 ; SOFTWARE: FASTEST for Windows Version 4.0  
 ; SEQ. ID NO: 13122  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthesized by Invitrogen, Inc.  
 US-10-215-112-13122

Query Match: 56.0%, Score 14; DB 15; Length 25;  
 Best Local Similarity: 77.3%, Freq. No. 3,1e+03;  
 Matches: 17; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;

QY 2 GTCCAGCTTACAAATGAGGT 23  
 |||||  
 DB 23 GTCCAGTACAGAGAAAGAGAG 2

RESULT 11  
 US-10-098-263B-45349/C  
 ; Sequence 45349, Application US/10098263B  
 ; Publication No. US0303141A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; CURRENT FILING DATE: 2002-07-08  
 ; PRIOR APPLICATION NUMBER: 09/276,759  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ. ID NOS: 11090  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1  
 ; SEQ. ID NO: 45349  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-45349

Query Match: 56.0%, Score 14; DB 15; Length 25;  
 Best Local Similarity: 77.3%, Freq. No. 3,1e+03;  
 Matches: 17; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;

QY 3 TCCGAGCCGAGAGAGATGAGGT 24  
 |||||  
 DB 24 TCCGAGTTATGATGAGAGAGAT 3

RESULT 12  
 US-10-098-263B-45350/C  
 ; Sequence 45350, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:  
 ; APPLICANT: Miltman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; CURRENT FILING DATE: 2002-07-08  
 ; PRIOR APPLICATION NUMBER: 09/276,759  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ. ID NOS: 13106  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1  
 ; SEQ. ID NO: 45350  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-45350

Query Match: 56.0%, Score 14; DB 15; Length 25;  
 Best Local Similarity: 77.3%, Freq. No. 3,1e+03;  
 Matches: 17; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;

QY 3 TCCGAGCCGAGAGAGATGAGGT 24  
 |||||  
 DB 24 TCCGAGTACAGAGAGAGAGAT 3

RESULT 13  
 US-09-755-830-19

; Sequence 19, Application US/09755830  
 ; Publication No. US0303233A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Georgopoulos, Kalia  
 ; TITLE OF INVENTION: LABS RESEARCH BY HYPHENED AND HAPS  
 ; FILE REFERENCE: 1998/067001  
 ; CURRENT APPLICATION NUMBER: US/09/755,830  
 ; CURRENT FILING DATE: 2001-01-05  
 ; PRIOR APPLICATION NUMBER: US 08/282,300  
 ; PRIOR FILING DATE: 1994-07-26  
 ; PRIOR APPLICATION NUMBER: US 08/238,212  
 ; PRIOR FILING DATE: 1994-05-02  
 ; PRIOR APPLICATION NUMBER: US 06/121,438  
 ; PRIOR FILING DATE: 1993-09-14  
 ; PRIOR APPLICATION NUMBER: US 07/316,233  
 ; PRIOR FILING DATE: 1992-09-14  
 ; NUMBER OF SEQ. ID NOS: 43  
 ; SOFTWARE: FASTEST for Windows Version 4.0  
 ; SEQ. ID NO: 19  
 ; LENGTH: 24  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthesitically generated primer  
 US-09-755-830-19

Query Match: 55.2%, Score 13.8; DB 11; Length 24;  
 Best Local Similarity: 59.2%, Freq. No. 3,1e+03;  
 Matches: 15; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

QY 1 GCTCGAGCCGAGAGAG 17  
 |||||  
 DB 5 GCTCGAGCCGAGAGAG 21

RESULT 14  
 US-10-098-263B-45351/C  
 ; Sequence 45351, Application US/10098263B  
 ; Publication No. US0303141A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; CURRENT FILING DATE: 2002-07-08  
 ; PRIOR APPLICATION NUMBER: 09/276,759  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ. ID NOS: 11090  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1  
 ; SEQ. ID NO: 45351  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-45351

Query Match: 55.2%, Score 13.8; DB 11; Length 24;  
 Best Local Similarity: 59.2%, Freq. No. 3,1e+03;  
 Matches: 15; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

QY 1 GCTCGAGCCGAGAGAG 17  
 |||||  
 DB 5 GCTCGAGCCGAGAGAG 21

RESULT 15  
 US-10-098-263B-45352/C  
 ; Sequence 45352, Application US/10098263B  
 ; Publication No. US0303141A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miltman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; CURRENT FILING DATE: 2002-07-08  
 ; PRIOR APPLICATION NUMBER: 09/276,759  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ. ID NOS: 11090  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1  
 ; SEQ. ID NO: 45352  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-45352



INFORMATION SOURCE: FBI/DOJ/00065  
PRIOR FILING DATE: 2001-01-30







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528 10.8 43.2 US 09-007 921-15 Sequence 15, Affi
529 10.8 43.2 Sequence 15, Affi
530 10.8 43.2 Sequence 15, Affi
531 10.8 43.2 Sequence 15, Affi
532 10.8 43.2 Sequence 15, Affi
533 10.8 43.2 Sequence 15, Affi
534 10.8 43.2 Sequence 15, Affi
535 10.8 43.2 Sequence 15, Affi
536 10.8 43.2 Sequence 15, Affi
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538 10.8 43.2 Sequence 15, Affi
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540 10.8 43.2 Sequence 15, Affi
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543 10.8 43.2 Sequence 15, Affi
544 10.8 43.2 Sequence 15, Affi
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598 10.8 43.2 Sequence 15, Affi
599 10.8 43.2 Sequence 15, Affi
600 10.8 43.2 Sequence 15, Affi
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C 90	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 54381, A	163	11.8	47.2	33	11	US-09-997-4865-72	Sequence 472, A
C 91	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47801, A	C 164	11.8	47.2	20	11	US-10-098-2638-54381	Sequence 47801, A
C 92	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47802, A	C 165	11.8	47.2	20	11	US-10-098-2638-54381	Sequence 47802, A
C 93	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47803, A	C 166	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47803, A
C 94	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47804, A	C 167	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47804, A
C 95	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47805, A	C 168	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47805, A
C 96	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47806, A	C 169	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47806, A
C 97	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47807, A	C 170	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47807, A
C 98	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47808, A	C 171	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47808, A
C 99	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47809, A	C 172	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47809, A
C 100	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47810, A	C 173	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47810, A
C 101	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47811, A	C 174	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47811, A
C 102	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47812, A	C 175	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47812, A
C 103	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47813, A	C 176	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47813, A
C 104	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47814, A	C 177	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47814, A
C 105	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47815, A	C 178	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47815, A
C 106	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47816, A	C 179	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47816, A
C 107	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47817, A	C 180	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47817, A
C 108	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47818, A	C 181	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47818, A
C 109	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47819, A	C 182	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47819, A
C 110	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47820, A	C 183	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47820, A
C 111	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47821, A	C 184	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47821, A
C 112	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47822, A	C 185	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47822, A
C 113	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47823, A	C 186	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47823, A
C 114	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47824, A	C 187	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47824, A
C 115	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 47825, A	C 188	11.8	47.2	23	12	US-09-997-4865-72	Sequence 47825, A
C 116	12.2	48.8	25.15	US-10-098-2638-54381	Sequence 4782							



US-09-313-932-24

Query Match 48.8%; Score 12.2; DB 4; Length 20;  
 Best Local Similarity 82.4%; Pred. No. 2.7e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 CCGAGAAAGATGAGCTC 25  
 |||||  
 CH 4 CCGAGATAGATGGGCTC 20

RESULT 40

US-09-313-932-93

? Sequence 93, Application US/09313932A  
 ? Patent No. 6228642  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Baker, Brenda  
 ? APPLICANT: Bennett, C. Frank  
 ? APPLICANT: Butler, Madeline M.  
 ? APPLICANT: Shanahan, William R.  
 ? TITLE OF INVENTION: ANTISENSE-INDUCED SELECTIVE MITIGATION OF THE-  
 ? TITLE OF INVENTION: EXPRESSION  
 ? FILE REFERENCE: ISPH-0356  
 ? CURRENT APPLICATION NUMBER: US/09/313,932A  
 ? CURRENT FILING DATE: 1999-05-18  
 ? NUMBER OF SEQ ID NOS: 501  
 ? SEQ ID NO 93  
 ? LENGTH: 20  
 ? TYPE: DNA  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthetic  
 US-09-313-932-93

Query Match 48.8%; Score 12.2; DB 4; Length 20;  
 Best Local Similarity 82.4%; Pred. No. 2.7e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 CCGAGAAAGATGAGCTC 25  
 |||||  
 CH 1 CCGAGATAGATGGGCTC 17

Search completed: July 21, 2003, 15:49:21  
 Job time : 26.1617 secs

FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME, FIRM, FARED FAY  
 REGISTRATION NUMBER: 34,950  
 REFERENCE/DOCKET NUMBER: 01,1229  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 302-993-7000  
 TELEFAX: 302-773-0164  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOTIF TYPE: other nucleic acid  
 DESCRIPTION: /desc = "primer"  
 HYDROTHERMAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: 5' E. coli DS primer  
 US-09-094-148-3

Query Match 100.0% Score 12.0 DB 3 Length 34  
 Best Local Similarity 92.4% Freq No. 2.7e+03  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY 1 CGTCCGAGCCCAAGATGAG 23  
 DB 23 CGTCCGAGCCCAAGATGAG 2

RESULT 36  
 US-09-167-109-38/c  
 Sequence 38, Application US/00106100A  
 Patent No. 6399297  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Brenda F.  
 APPLICANT: Cozzelli, Lex M.  
 APPLICANT: Monia, Brett P.  
 APPLICANT: Xu, Xiaohua S.  
 TITLE OF INVENTION: ANTISENSE MODULATION OF TGF EXPRESSION  
 FILE REFERENCE: ISPH-0321  
 CURRENT APPLICATION NUMBER: US/00106100A  
 CURRENT FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 20  
 SEQ ID NO 38  
 LENGTH: 18  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: antisense sequence  
 US-09-167-109-38

Query Match 100.0% Score 12.0 DB 3 Length 18  
 Best Local Similarity 92.4% Freq No. 2.7e+03  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY 1 CGTCCGAGCCCAAGATGAG 17  
 DB 18 CGTCCGAGCCCAAGATGAG 2

RESULT 37  
 US-09-166-186-24  
 Sequence 24, Application US/00106100A  
 Patent No. 6399290  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Brenda  
 APPLICANT: Bennett, C. Frank  
 APPLICANT: Butler, Madeline M.  
 APPLICANT: Shanahan, William R.  
 TITLE OF INVENTION: ANTISENSE Oligonucleotide MODULATION OF TGF EXPRESSION

FILE REFERENCE: ISPH-0322  
 CURRENT APPLICATION NUMBER: US/00106100A  
 CURRENT FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 250  
 SEQ ID NO 24  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: antisense sequence  
 US-09-166-186-24

Query Match 48.8% Score 12.0 DB 3 Length 20  
 Best Local Similarity 52.4% Freq No. 2.7e+03  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY 5 CCGAGAAATGAGTGC 25  
 DB 4 CCGAGAAATGAGTGC 20

RESULT 38  
 US-09-166-186-93  
 Sequence 93, Application US/00106100A  
 Patent No. 6060580  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Brenda  
 APPLICANT: Bennett, C. Frank  
 APPLICANT: Butler, Madeline M.  
 APPLICANT: Shanahan, William R.  
 TITLE OF INVENTION: ANTISENSE Oligonucleotide MODULATION OF TGF EXPRESSION  
 FILE REFERENCE: ISPH-0322  
 CURRENT APPLICATION NUMBER: US/00106100A  
 CURRENT FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 250  
 SEQ ID NO 93  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: antisense sequence  
 US-09-166-186-93

Query Match 48.8% Score 12.0 DB 3 Length 20  
 Best Local Similarity 52.4% Freq No. 2.7e+03  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY 9 CCGAGAAATGAGTGC 25  
 DB 1 CCGAGAAATGAGTGC 17

RESULT 39  
 US-09-313-932-24  
 Sequence 24, Application US/00106100A  
 Patent No. 6399294  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Brenda  
 APPLICANT: Bennett, C. Frank  
 APPLICANT: Butler, Madeline M.  
 APPLICANT: Shanahan, William R.  
 TITLE OF INVENTION: ANTISENSE Oligonucleotide MODULATION OF TGF EXPRESSION  
 FILE REFERENCE: ISPH-0356  
 CURRENT APPLICATION NUMBER: US/00106100A  
 CURRENT FILING DATE: 1999-01-18  
 NUMBER OF SEQ ID NOS: 501  
 SEQ ID NO 24  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: synthetic

```

Sequence 37, Application FC/TUS9507068
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS FOR DETECTING MUTATIONS ASSOCIATED WITH
TITLE OF INVENTION: HYPERTROPHIC CALCIUM PATHWAY
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 110
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 127/05/95/07068
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/354,326
FILING DATE: 12-DEC-1994
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/050,627
FILING DATE: 12-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,595
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CTS
LOCATION: 1..12
PRT US95-07068-37
Query Match 49.6%; Score 12.4; DB 5; Length 32;
Best local similarity 22.93; First 31; 33-93;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0,
CY 11 CAGAAATATGAGT 24
DB 1 CAGAAATATGAGT 14
RESULT 34
US-08-577-081A-45
Sequence 45, Application US/09094148
GENERAL INFORMATION:
APPLICANT: Yang, Soo Young
APPLICANT: Gersh, Nezhil
TITLE OF INVENTION: Methods and polynucleotides for typing HLA
TITLE OF INVENTION: Class I genes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cepheid & Larson
STREET: 1332 Commodore Street Suite 300
CITY: Yorktown
STATE: NY

```

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COUNTRY: US
ZIP: 10598
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Mold Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 12/09/95/11,081A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 34
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE: human
ORGANISM: human
FEATURE:
OTHER INFORMATION: locus specific amplification primer for
US-08-577-081A-45
Query Match 49.6%; Score 12.4; DB 3; Length 34;
Best local similarity 72.78; First 30; 2,46-103;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0,
CY 2 GTCTAGCCCAAGAGAGATG 23
DB 5 GTCTAGCCCAAGAGAGATG 26
RESULT 35
US-09-094-148-3/C
Sequence 3, Application US/09094148
GENERAL INFORMATION:
APPLICANT: BAEGT, KAREN ONLEY
APPLICANT: JORGAN, DOUGLAS BRIAN
APPLICANT: VITAMEN, PAUL VEIKKO
TITLE OF INVENTION: 3,4-DIHYDROXY 2 BUTANONE
TITLE OF INVENTION: 4-PHOSPHATE SYNTHASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,148

```

SOFTWARE: Patent in place #1.0, Version #1.20  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-09/774,337  
 FILING DATE: 21-AUG-1991  
 CLASSIFICATION: 424  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 09/074,000/000  
 FILING DATE: 23-FEB-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gale, Edwin J.  
 REGISTRATION NUMBER: 28,584  
 REFERENCE TO PRT NUMBER: 17941  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (613) 237-6900  
 TELEFAX: (613) 237-0045  
 INFORMATION FOR SEQ. ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYDROTHERMAL: NO  
 ANTI-SENSE: NO  
 US-09/774,337-13

Query Match 49.6% Score 12.4; DB 2; Length 32;  
 Best Local Similarity 32.0% Pred. No. 2.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 TCGAGGCGCAGAGATGAGCT 24  
 DB 27 TCGAGGCGCAGAGATGAGCT 6

RESULT 31  
 US-08-481,793-37  
 Sequence 37: Application US-08/481,793  
 Patent No. 5840477  
 GENERAL INFORMATION:  
 APPLICANT: SEIDMAN, C.E. ET AL.  
 TITLE OF INVENTION: METHODS FOR DETECTING MUTATIONS ASSOCIATED WITH  
 TITLE OF INVENTION: HYPERTROPHIC CARDIOMYOPATHY  
 NUMBER OF SEQUENCES: 48  
 ADDRESS/AGENT ADDRESS:  
 ADDRESSER: LAMIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 TELEFAX: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: EMM/MS-DOS  
 SOFTWARE: ASCII text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/084,941/793  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/054,326  
 FILING DATE: 12-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HANLEY, ELIZABETH A.  
 REGISTRATION NUMBER: 33,505  
 REFERENCE/DOCKET NUMBER: 131-037  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ. ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 base pairs

TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..12  
 US-08-481,793-37

Query Match 49.6% Score 12.4; DB 2; Length 32;  
 Best Local Similarity 32.0% Pred. No. 2.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 11 CAGAAATATGAGCT 24  
 DB 1 CAGAAATATGAGCT 14

RESULT 32  
 US-08-354-326-37  
 Sequence 37: Application US-08/354,326  
 Patent No. 5842121  
 GENERAL INFORMATION:  
 APPLICANT: SEIDMAN, C.E. ET AL.  
 TITLE OF INVENTION: METHODS FOR DETECTING MUTATIONS ASSOCIATED WITH  
 TITLE OF INVENTION: HYPERTROPHIC CARDIOMYOPATHY  
 NUMBER OF SEQUENCES: 48  
 ADDRESS/AGENT ADDRESS:  
 ADDRESSER: LAMIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: ASCII text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/054,326  
 FILING DATE: 01-JUN-1994  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/054,326  
 FILING DATE: 01-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HANLEY, ELIZABETH A.  
 REGISTRATION NUMBER: 33,505  
 REFERENCE/DOCKET NUMBER: 131-037  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ. ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..12  
 US-08-354-326-37

Query Match 49.6% Score 12.4; DB 2; Length 32;  
 Best Local Similarity 32.0% Pred. No. 2.3e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 11 CAGAAATATGAGCT 24  
 DB 1 CAGAAATATGAGCT 14

RESULT 33  
 PCT-US-95-07668-37



RESULT 30  
 US-07-743-357-13/C  
 Sequence 13, Application Us/0702361  
 Patent No. 6329516  
 GENERAL INFORMATION:  
 APPLICANT: Halling, Blak  
 TITLE OF INVENTION: Lipid-protein GABA gated channel  
 TITLE OF INVENTOR: Chantrel  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Decarte Price & Friends  
 STREET: 447 Lawrence Drive, Building 3, Suite 210  
 CITY: Lawrenceville  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08543  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: PASSED FOR WINDOWS Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 07/02361  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bloom, Allen  
 REGISTRATION NUMBER: 29,135  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-520 3214  
 TELEFAX: 609 520 3259  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-002-361-13  
 Query Match: 49.4% Score 12.4; DB 4; Length 28;  
 Best Local Similarity 66.7%; Freq. NO. 2.1e+01;  
 Matches 12; Conservative 4; Mismatches 2; Indels 1; Shifts 0  
 CY 4 CCGAGGCGGAGAGATCA 21  
 ||||| ||||| |||||  
 DB 1 CCGAGGCGGAGATCA 18

STREET: 126 East Lincoln Avenue, P.O. Box 2000-0907  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-IBM/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/458,067  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Giessey, Joanne M.  
 REGISTRATION NUMBER: 32,838  
 REFERENCE/DOCKET NUMBER: 19457  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-3046  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 29 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 US-09-458-067-27  
 Query Match: 50.4% Score 12.6; DB 1; Length 29;  
 Best Local Similarity: 78.9%; Freq. No. 1; Seq-ID: 3;  
 Matches: 15; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

RESULT 26  
 PCT-US96-07796-27  
 Sequence 27, Application PC/TUS9607795  
 GENERAL INFORMATION:  
 APPLICANT: MPECK & CO., INC.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Giessey, Joanne M.  
 REGISTRATION NUMBER: 32,838  
 REFERENCE/DOCKET NUMBER: 19457  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-3046  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 29 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 US-09-458-067-27

Query Match: 50.4% Score 12.6; DB 1; Length 29;  
 Best Local Similarity: 78.9%; Freq. No. 1; Seq-ID: 3;  
 Matches: 15; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

DB 1  
 2 GTCGAGCCCGAAGATG 20  
 3 GATCGAGCCCGAAGATG 21

RESULT 26  
 PCT-US96-07796-27  
 Sequence 27, Application PC/TUS9607795  
 GENERAL INFORMATION:  
 APPLICANT: MPECK & CO., INC.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Giessey, Joanne M.  
 REGISTRATION NUMBER: 32,838  
 REFERENCE/DOCKET NUMBER: 19457  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-3046  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 29 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 US-09-458-067-27

Query Match: 50.4% Score 12.6; DB 1; Length 29;  
 Best Local Similarity: 78.9%; Freq. No. 1; Seq-ID: 3;  
 Matches: 15; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

DB 1  
 2 GTCGAGCCCGAAGATG 20  
 3 GATCGAGCCCGAAGATG 21

INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 29 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 PCT-US96-07796-27  
 Query Match: 50.4% Score 12.6; DB 5; Length 29;  
 Best Local Similarity: 78.9%; Freq. No. 1; Seq-ID: 3;  
 Matches: 15; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

DB 1  
 2 GTCGAGCCCGAAGATG 20  
 3 GATCGAGCCCGAAGATG 21

RESULT 27  
 PCT-US96-07796-27  
 Sequence 27, Application PC/TUS9607796  
 GENERAL INFORMATION:  
 APPLICANT: MPECK & CO., INC.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Giessey, Joanne M.  
 REGISTRATION NUMBER: 32,838  
 REFERENCE/DOCKET NUMBER: 19457  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-3046  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 29 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 PCT-US96-07796-27

Query Match: 50.4% Score 12.6; DB 5; Length 29;  
 Best Local Similarity: 78.9%; Freq. No. 1; Seq-ID: 3;  
 Matches: 15; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

DB 1  
 2 GTCGAGCCCGAAGATG 20  
 3 GATCGAGCCCGAAGATG 21

RESULT 28  
 US-09-538-875-12



APPLICATION NUMBER: FR 94/05641  
FILING DATE: 06-MAY-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: FR 94/05641  
FILING DATE: 06-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: PATCH, Andrew J.  
REGISTRATION NUMBER: 31,025  
REFERENCE/DOCKET NUMBER: RET 26/244  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-521-2297  
TELEFAX: 703-695-0673  
TELEX: 349478 EPRN  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-737-271-7

Query Match 51.2% Score 12.8 DB 2 Length 35  
Best Local Similarity 70.8% Ident No. 1  
Matches 17, Conservative 0, Mismatches 7, Indels 0  
CY 1 CGTCCGAGCCCGAGAGATGAGT 24  
DB 7 CGACTTACCCAGAGACGATGAGT 30

RESULT 20  
US-09-058-555-7  
Sequence 7, Application 09/0909775  
Patent No. 6143273  
GENERAL INFORMATION:  
APPLICANT: FAURE, Florence  
APPLICANT: HERGEN, Thierry  
APPLICANT: HUARD, Bertrand  
APPLICANT: TRIEBEL, Frederic  
TITLE OF INVENTION: SITE SPECIFIC REACTIONS OF THE  
TITLE OF INVENTION: CAG33 PROTEIN PRODUCTION METHOD, HEREDITARY COMPOSITION,  
TITLE OF INVENTION: ANTI-HEREDITARY ANTIBODIES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: YOUNG & THOMPSON  
STREET: 745 South 23rd Street  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-09-058-555  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US-09-058-555  
FILING DATE: 24-DEC-1996  
APPLICATION NUMBER: FR 94/05641  
FILING DATE: 06-MAY-1994  
PRIOR APPLICATION DATA:  
AFFILIATION NUMBER: FCT/FA/000002  
FILING DATE: 06-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: PATCH, Andrew J.  
REGISTRATION NUMBER: 31,025  
REFERENCE/DOCKET NUMBER: RET 26/244  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-521-2297  
TELEFAX: 703-695-0573  
TELEX: 349478 EPRN  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-058-555-7

Query Match 51.2% Score 12.8 DB 3 Length 35  
Best Local Similarity 70.8% Ident No. 1  
Matches 17, Conservative 0, Mismatches 7, Indels 0  
CY 1 CGTCCGAGCCCGAGAGATGAGT 24  
DB 7 CGACTTACCCAGAGACGATGAGT 30

RESULT 21  
US-09-359-757-14/C  
Sequence 14, Application 09/0909757  
Patent No. 6060546  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: William Gaarde  
APPLICANT: Lex M. Cowart  
TITLE OF INVENTION: ANTISENSE REGULATION OF NERVE EXPRESSION  
FILE REFERENCE: RUS-0078  
CURRENT APPLICATION NUMBER: US-09-359-757  
CURRENT FILING DATE: 1999-07-23  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 14  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense oligonucleotide  
US 09 359 757-14

Query Match 50.4% Score 12.6 DB 2 Length 20  
Best Local Similarity 79.5% Ident No. 1  
Matches 15, Conservative 0, Mismatches 4, Indels 0  
CY 4 CGAGCTCTGAGAGATGAG 22  
DB 19 CCGGCGCCGAGAGATGAG 1

RESULT 22  
US-09-458-067-26/C  
Sequence 2, Application 09/0909467  
Patent No. 572857  
GENERAL INFORMATION:  
APPLICANT: Register, Robert B.  
APPLICANT: Shafer, Jules A.  
TITLE OF INVENTION: HERFED SIMPLEX TYPE 1 PROTEASE MUTANTS  
TITLE OF INVENTION: ANT-VEGFRS  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Ms. Joanne M. Giesler  
STREET: 174 East 111th St  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30

```

STATE: Kyungki-do
COUNTRY: Republic of Korea
ZIP: 423-060
ADDRESSEE: Shin, Nam-Kyu
STREET: #181 404 Salsang 4 Bldg, Tongjak-ku
CITY: Seoul
STATE:
COUNTRY: Republic of Korea
ZIP: 156-094
ADDRESSEE: Lee, Inkyung
STREET: 11/2, #302 19 Deam 4 Bldg, Nam-ku
CITY: Incheon
STATE:
COUNTRY: Republic of Korea
ZIP: 402-204
ADDRESSEE: Krog, Sungsun
STREET: #84 4 Daeshin-dong, Seodaemun-ku
CITY: Seoul
STATE:
COUNTRY: Republic of Korea
ZIP: 128-108
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5inch 2.0MB storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/09/38, 576
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/193, 336
FILING DATE:
APPLICATION NUMBER: KR 93-1751
FILING DATE: 9-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/POCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 bases
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: primer DNA
US-08-538-875-57

Query Match 51.2% Score 12.9; DB 1; Length 22;
Post Local Similarity 40.8; Freq No. 14;
Matches 14; Conservativity 0; Mismatches 0; Indels 0; Gaps 0
2Y 10 CCAGAACATGAGATG 25
18 CCAGAACATGAGATG 3
Db 18 CCAGAACATGAGATG 3

RESULT 18
US-08-117-952-501
Sequence 501, Application US/08/17952
Patent No. 5681760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR SEPARATION OF SEQUENCE
TITLE OF INVENTION: SEPARATION MAPS OF COMPLEX GENOMES
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSER: Preety, Schroeder, Pringmann & Glavin
STREET 444 South Flower Street, Suite 1000

```

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CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117, 952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078, 471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen R.
REGISTRATION NUMBER: 31,192
REFERENCE/POCKET NUMBER: 041 9473
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 501:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Oligonucleotide
HYPOTHEetical: NO
ANTI-SENSE: NO
US-08-117-952-501

Query Match 51.4% Score 12.6; DB 2; Length 30;
Post Local Similarity 70.8; Freq. No. 150493;
Matches 17; Conservativity 0; Mismatches 7; Indels 0; Gaps 0
2Y 2 GTCCAGCCAGAACATGAGATG 25
Db 2 GTCCAGCCAGAACATGAGATG 10

RESULT 19
US-08-737-271-7
Sequence 7, Application US/08/737271
Patent No. 5955300
GENERAL INFORMATION:
APPLICANT: FAURE, Florence
APPLICANT: HERCEND, Thierry
APPLICANT: HUARD, Bertrand
APPLICANT: TRIBEL, Frederic
TITLE OF INVENTION: METHOD FOR IDENTIFYING FEATURES OF THE
TITLE OF INVENTION: DNA / 15-GENE, IDENTIFYING AND DIFFERENTIATING OF MUTATIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: YOUNG & THOMPSON
STREET 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737, 271
FILING DATE: 04-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

```

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1 TITLE OF INVENTION: IDENTIFIED PROTEIN
2 FILE REFERENCE: IDENTIFIED PROTEIN
3 CURRENT APPLICATION NUMBER: 1999-05-06
4 CURRENT FILING DATE: 1999-05-06
5 PRIOR APPLICATION NUMBER: 98108210
6 NUMBER OF SEQ. ID NOS.: 42
7 SOFTWARE: Patent In Ver. 2.1
8 SEQ. ID NO. 12
9 LENGTH: 24
10 TYPE: DNA
11 ORGANISM: Artificial Sequence
12 FEATURE:
13 OTHER INFORMATION: Description of Artificial Sequence: Sense Primer
14 OTHER INFORMATION: 5' to 3' direction: 5' to 3' direction: 5' to 3'
15 US-09-106-595-132

Query Match: 52.0% Score: 132 DB 4, Length: 26
Best Local Similarity: 76.2% Filed: No. 1229-023
Matches: 169 Conservative: 0 Mismatch: 53 Indels: 0 Gaps: 0

QY 1 CCGGAGGCGGCAAGGAGGCA 21
DB 6 CCGGAGGCGGCAAGGAGGCA 26

RESULT 15
US-08-686-968C-47
1 Sequence 47: Application US/08686968C
2 Patent No. 7203921
3 GENERAL INFORMATION:
4 APPLICANT: Gochang, Mark D.
5 APPLICANT: Gochang, David E.
6 TITLE OF INVENTION: Polynuclear Oligonucleotide
7 FILE REFERENCE: 39119-H/JML
8 CURRENT APPLICATION NUMBER: 98108210
9 CURRENT FILING DATE: 1998-07-25
10 NUMBER OF SEQ. ID NOS.: 21
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ. ID NO. 47
13 LENGTH: 33
14 TYPE: DNA
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence: Primer
18 US-08-686-968C-47

Query Match: 52.0% Score: 132 DB 4, Length: 33
Best Local Similarity: 76.2% Filed: No. 1229-023
Matches: 169 Conservative: 0 Mismatch: 53 Indels: 0 Gaps: 0

QY 3 TCCGAGGCGGCAAGGAGGCA 21
DB 7 TCCGAGGCGGCAAGGAGGCA 27

RESULT 16
US-08-538-875-55/C
1 Sequence 55: Application US/08538875
2 Patent No. 5773582
3 GENERAL INFORMATION:
4 APPLICANT: Shin, Hany-Cheol
5 APPLICANT: Shin, Nam Kyu
6 APPLICANT: Lee, Inkyung
7 APPLICANT: Kang, Sungzong
8 TITLE OF INVENTION: Tumor Necrosis Factor Receptor
9 NUMBER OF SEQUENCES: 73
10 CORRESPONDING ADDRESS:
11 ADDRESSEE: Shin, Hany-Cheol
12 STREET: 44-14 Gyeonggi Apt. 1014 800, Haan-dong
13 CITY: Kwangmyung-shi
14 STATE: Kwangmyung-shi
15 COUNTRY: Republic of Korea

```

```

1 CITY: 422-060
2 ADDRESSEE: Shin, Nam Kyu
3 STREET: #12-434 Chang 4 Bldg, Bujong-ku
4 CITY: Seoul
5 STATE:
6 COUNTRY: Republic of Korea
7 CITY: 156-034
8 ADDRESSEE: Lee, Inkyung
9 STREET: 11/2, #100-33 Chang 4 Bldg, Nam-ku
10 CITY: Incheon
11 STATE:
12 COUNTRY: Republic of Korea
13 ZIP: 402-204
14 ADDRESSEE: Kang, Sungzong
15 STREET: #24 4 Bldg, 1014, Gyeonggi-ku
16 CITY: Seoul
17 STATE:
18 COUNTRY: Republic of Korea
19 ZIP: 150-160
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Diskette 3.5inch 2.0mb storage
22 COMPUTER: IBM PC/AT
23 OPERATING SYSTEM: MS-DOS
24 SOFTWARE: WordPerfect 5.1
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08-132,875
27 FILING DATE:
28 CLASSIFICATION: 435
29 INKIC APPLICATION DATA:
30 APPLICATION NUMBER: US/08-132,875
31 FILING DATE:
32 APPLICATION NUMBER: 98-23-1701
33 FILING DATE: 9-FEB-1993
34 ATTORNEY/AGENT INFORMATION:
35 NAME:
36 REGISTRATION NUMBER:
37 REFERENCE/LOCAL NUMBER:
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE:
40 TELEFAX:
41 INFORMATION FOR SEQ. ID NO. 55:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 22 bases
44 TYPE: nucleic acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47 MOLECULE TYPE: primer DNA
48 US-08-538-875-55

Query Match: 51.2% Score: 115 DB 1, Length: 121
Best Local Similarity: 87.5% Filed: No. 1,46+033
Matches: 141 Conservative: 0 Mismatch: 0 Indels: 0 Gaps: 0

QY 19 CCGGAGGCGGCAAGGAGGCA 25
DB 18 CCGGAGGCGGCAAGGAGGCA 3

RESULT 17
US-08-538-875-57/C
1 Sequence 57: Application US/08538875
2 Patent No. 5773582
3 GENERAL INFORMATION:
4 APPLICANT: Shin, Hany-Cheol
5 APPLICANT: Shin, Nam Kyu
6 APPLICANT: Lee, Inkyung
7 APPLICANT: Kang, Sungzong
8 TITLE OF INVENTION: Tumor Necrosis Factor Receptor
9 NUMBER OF SEQUENCES: 73
10 CORRESPONDING ADDRESS:
11 ADDRESSEE: Shin, Hany-Cheol
12 STREET: 44-14 Gyeonggi Apt. 1014 800, Haan-dong
13 CITY: Kwangmyung-shi

```







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US-08-442-134A-6
Sequence 6, Application US/08442134A
Patent No. 5696088
GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harder, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: RNA Encoding the Human F2U Receptor and
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: North Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
FILING DATE: 16 MAY 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/442,134A
FILING DATE: 16 MAY 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2000
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-442-134A-6
Query Match 53.0% Score 13.4, DB: 1, Length 30,
Best Local Similarity 56.0% Freq. No. 7, 6e+02
Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0
1 GCTGCAAGCTGCAAAATGATGCTG 25
|||||:|||||:|||||
3 GCTGCAAGCTGCAAAATGATGCTG 27

```

```

ADDRESS: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: North Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
FILING DATE: 16 MAY 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/442,134A
FILING DATE: 16 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2000
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-442-581B-6
Query Match 53.0% Score 13.4, DB: 1, Length 30,
Best Local Similarity 56.0% Freq. No. 7, 6e+02
Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0
1 GCTGCAAGCTGCAAAATGATGCTG 25
|||||:|||||:|||||
3 GCTGCAAGCTGCAAAATGATGCTG 27

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GENERAL INFORMATION
APPLICANT: GENESEE, KATHA A.
TITLE OF INVENTION: LAMIVUDINE DERIVATIVES AND COMPOSITIONS
NUMBER OF SEQUENCE: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: LAMIV & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/238,212
FILING DATE: 14-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/121,438
FILING DATE: 03 MAY 94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/121,438
FILING DATE: 14-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/346,033
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/COCKET NUMBER: MFT 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-283-300A 19

Query Match      55.2%, Score 13.9, DB 4, Length 24,
Best Local Similarity 59.2%, First No. 4,7e+02,
Matches 15, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 1 CGTCCAGAGGATGAGAT 17
DB 5 GTTCTAGAGGATGAGAT 17

RESULT 5
PCT-0995-09345-19
Sequence 19, Application PCT/US9509345
GENERAL INFORMATION:
APPLICANT: GENESEE, KATHA A.
TITLE OF INVENTION: LAMIVUDINE DERIVATIVES AND COMPOSITIONS
NUMBER OF SEQUENCE: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: LAMIV & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:

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```

APPLICATION NUMBER: US 09/238,212
FILING DATE: 14-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/121,438
FILING DATE: 03 MAY 94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/121,438
FILING DATE: 14-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/346,033
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/COCKET NUMBER: MFT 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-0995-09345-19

Query Match      55.2%, Score 13.8, DB 5, Length 24,
Best Local Similarity 59.2%, First No. 4,7e+02,
Matches 15, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 1 CGTCCAGAGGATGAGAT 17
DB 5 GTTCTAGAGGATGAGAT 17

RESULT 6
US-09-452-624A-10
Sequence 10, Application US/09452624A
Patent No. 6428985
GENERAL INFORMATION:
APPLICANT: Broadex, Jonathan S.
ATTORNEY: Ding, Yao Zhong
ADDRESSER: 390 Li Hui
TITLE OF INVENTION: LAMIVUDINE DERIVATIVES AND COMPOSITIONS
FILE REFERENCE: UMIC:016P22
CURRENT APPLICATION NUMBER: US 09/452,624A
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 10
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-452-624A-10

Query Match      55.2%, Score 13.4, DB 4, Length 24,
Best Local Similarity 59.2%, First No. 4,7e+02,
Matches 14, Conservative 0, Mismatches 1, Indels 0, Gaps 0

CY 10 CGGAAAGATGAGAT 24
DB 4 CGGAAAGATGAGAT 18

RESULT 7

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C 977 10 40.0 26 1 US-08-416-241-44  
 C 978 10 40.0 26 2 US-08-416-273-35  
 C 979 10 40.0 26 2 US-08-244-122-17  
 C 980 10 40.0 26 2 US-08-113-024-35  
 C 981 10 40.0 26 2 US-08-244-124-4  
 C 982 10 40.0 26 2 US-08-417-226-35  
 C 983 10 40.0 26 2 US-08-116-444-74  
 C 984 10 40.0 26 2 US-08-196-131-35  
 C 985 10 40.0 26 2 US-08-643-732-35  
 C 986 10 40.0 26 2 US-08-416-137-35  
 C 987 10 40.0 27 1 US-08-029-402-12  
 C 988 10 40.0 27 1 US-08-143-219-20  
 C 989 10 40.0 27 1 US-08-416-241-44  
 C 990 10 40.0 27 2 US-08-292-597-58  
 C 991 10 40.0 27 2 US-08-344-653-58  
 C 992 10 40.0 27 2 US-08-473-685-58  
 C 993 10 40.0 27 2 US-08-256-426P-255  
 C 994 10 40.0 27 2 US-08-483-888-58  
 C 995 10 40.0 27 2 US-08-087-116-54  
 C 996 10 40.0 27 2 US-08-411-844-25  
 C 997 10 40.0 27 2 US-08-157-253-58  
 C 998 10 40.0 27 2 US-08-157-253-58  
 C 999 10 40.0 27 2 US-08-087-811-58  
 C 1000 10 40.0 27 2 US-08-087-811-58

## ALIGNMENTS

## RESULT 1

US-09-489-765A-31/2  
 Sequence 31: Application US/09489765A

Patent No. 6121029  
 GENERAL INFORMATION:  
 APPLICANT: Madeline M. Butler  
 APPLICANT: Robert McKay  
 APPLICANT: Brett P. Monia  
 APPLICANT: Jacqueline Wyatt  
 TITLE OF INVENTION: ANTIBODIES THAT INHIBIT THE SYNTHESIS OF SYNTHASE KINASE 3 PETA EXHIBIT  
 FILE REFERENCE: RTO 0124  
 CURRENT APPLICATION NUMBER: US/09/489,765A  
 CURRENT FILING DATE: 2000-01-19  
 NUMBER OF SEQ ID NOS: 85  
 SEQ ID NO 31  
 LENGTH: 23  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense oligonucleotide  
 US-09-489-765A-31

Query Match: 56.0% Score 14, DB 4, Length 20  
 Best Local Similarity: 100.0%, Fnd. No. 3, 66+02  
 Matches: 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0

RESULT 2  
 US-09-489-765A-12/2  
 Sequence 12: Application US/09489765A  
 Patent No. 6121029  
 GENERAL INFORMATION:  
 APPLICANT: Madeline M. Butler  
 APPLICANT: Robert McKay  
 APPLICANT: Brett P. Monia  
 APPLICANT: Jacqueline Wyatt  
 TITLE OF INVENTION: ANTIBODIES THAT INHIBIT THE SYNTHESIS OF SYNTHASE KINASE 3 PETA EXHIBIT  
 FILE REFERENCE: RTO 0124  
 CURRENT APPLICATION NUMBER: US/09/489,765A  
 CURRENT FILING DATE: 2000-01-19

NUMBER OF SEQ ID NOS: 85  
 SEQ ID NO 32  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense oligonucleotide  
 US-09-489-765A-12

Query Match: 56.0% Score 14, DB 4, Length 20  
 Best Local Similarity: 100.0%, Fnd. No. 3, 66+02  
 Matches: 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0

C 1 10 40.0 26 1  
 C 2 10 40.0 26 2  
 C 3 10 40.0 26 2  
 C 4 10 40.0 26 2  
 C 5 10 40.0 26 2  
 C 6 10 40.0 26 2  
 C 7 10 40.0 26 2  
 C 8 10 40.0 26 2  
 C 9 10 40.0 26 2  
 C 10 10 40.0 26 2  
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 C 85 10 40.0 26 2

## RESULT 3

US-08-707-743-11  
 Sequence 11: Application US/0807743

Patent No. 6063983  
 GENERAL INFORMATION:  
 APPLICANT: George J. Kalia  
 TITLE OF INVENTION: Methods of Use  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAMIVE & COCKFIELD  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/067,743  
 FILING DATE:  
 FRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/003,225  
 FILING DATE: 05-SEPT-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Myers, Louis  
 REGISTRATION NUMBER: 35,965  
 REFERENCE/DOCKET NUMBER: MGP-036CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-2400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-707-743-11

US-08-707-743-11

Query Match: 55.2% Score 13.8, DB 3, Length 24  
 Best Local Similarity: 88.2%, Fnd. No. 4, 76+02  
 Matches: 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0

C 1 10 40.0 26 1  
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 C 84 10 40.0 26 2  
 C 85 10 40.0 26 2

RESULT 4  
 US-08-283-400A-19  
 Sequence 19: Application US/0808283400A  
 Patent No. 6122278













[illegible]







```

Best local similarity: 100.0%, From: Max: 130.0%
Matches: 13; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 11 CACAAAGATGAGG 23
   |||||
DB 13 CAGAAAGATGAGG 1

RESULT 38
AAQ24564
ID AAQ24564 standard; DNA; 29 BP.
XX
AC AAQ24564;
XX
DT 26 NOV-1992 (first entry)
XX
DE NANBH peptide A primer 2.
XX
KM Beta (a1) expression vector; polynucleotide chain reaction; antigen;
XX PCR; antibody; peptide B, ss.
XX
OS Non A, non B hepatitis virus.
XX
PN JP04121193 A.
XX
PD 22-APR-1992.
XX
PE 07 SEP-1992; 90BP 0248412.
XX
PF 07 SEP-1992; 90BP 0248412.
XX
PV (KANA) KAGACATGCGAT KAGACATGCGAT
XX
DB WPI, 1992 188068473
XX
PT New non A, non B hepatitis virus fused peptide - useful as
PT antibody assay reagent for NANBH as it retains both
PT antigenicities and increases detection percentage.
XX
PS (nucleotide) 413 5' ATTT. 3'GAGGCG.
XX
XX The sequence from the AACGATG 4 are PCR primers which are used to
XX amplify the DNA which encodes peptide A from the non-A, non-B
XX hepatitis virus (NANBH) (see also AACGATG). Peptide A can be fused
XX to peptide B (see also AACGATG). Thus, the DNA encoding a novel
XX peptide (see also AACGATG). This novel peptide can be linked to a
XX carrier molecule, fused to a beta gal, the novel peptide-beta gal fusion
XX retains the antigenicity of both components and can be used in the
XX detection of NANBH. The DNA encoding the novel peptide can be
XX integrated into an expression vector and this can be used to
XX transform a host cell which can be cultured to express the peptide.
XX This novel peptide can be used as an antigen in an assay method to
XX detect NANBH antibody.
XX
SQ Sequence 29 BP; 6 A; 10 C; 12 G; 1 T; 0 other;
QY Query Match 52.0%; Score 13; DB 13; Length 29;
Best local similarity: 76.2%; From: 130.0%;
Matches: 16; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;
QY 3 TCTGACGCTCAGAAAGATGAGG 23
   |||||
DB 2 TCTGACGCTCAGAAAGATGAGG 22

RESULT 39
AAQ26169
ID AAQ26169 standard; DNA; 33 BP.
XX
AC AAQ26169;
XX
DT 24 JUL-1998 (first entry)
XX

```

```

XX
XX Best local similarity: 100.0%, From: Max: 130.0%
XX Matches: 13; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
XX QY 11 CACAAAGATGAGG 23
XX    |||||
XX DB 13 CAGAAAGATGAGG 1
XX
XX RESULT 38
XX AAQ24564
XX ID AAQ24564 standard; DNA; 29 BP.
XX XX
XX AC AAQ24564;
XX XX
XX DT 26 NOV-1992 (first entry)
XX XX
XX DE NANBH peptide A primer 2.
XX XX
XX KM Beta (a1) expression vector; polynucleotide chain reaction; antigen;
XX XX PCR; antibody; peptide B, ss.
XX XX
XX OS Non A, non B hepatitis virus.
XX XX
XX PN JP04121193 A.
XX XX
XX PD 22-APR-1992.
XX XX
XX PE 07 SEP-1992; 90BP 0248412.
XX XX
XX PF 07 SEP-1992; 90BP 0248412.
XX XX
XX PV (KANA) KAGACATGCGAT KAGACATGCGAT
XX XX
XX DB WPI, 1992 188068473
XX XX
XX PT New non A, non B hepatitis virus fused peptide - useful as
XX PT antibody assay reagent for NANBH as it retains both
XX PT antigenicities and increases detection percentage.
XX XX
XX PS (nucleotide) 413 5' ATTT. 3'GAGGCG.
XX XX
XX XX The sequence from the AACGATG 4 are PCR primers which are used to
XX XX amplify the DNA which encodes peptide A from the non-A, non-B
XX XX hepatitis virus (NANBH) (see also AACGATG). Peptide A can be fused
XX XX to peptide B (see also AACGATG). Thus, the DNA encoding a novel
XX XX peptide (see also AACGATG). This novel peptide can be linked to a
XX XX carrier molecule, fused to a beta gal, the novel peptide-beta gal fusion
XX XX retains the antigenicity of both components and can be used in the
XX XX detection of NANBH. The DNA encoding the novel peptide can be
XX XX integrated into an expression vector and this can be used to
XX XX transform a host cell which can be cultured to express the peptide.
XX XX This novel peptide can be used as an antigen in an assay method to
XX XX detect NANBH antibody.
XX XX
XX SQ Sequence 29 BP; 6 A; 10 C; 12 G; 1 T; 0 other;
XX QY Query Match 52.0%; Score 13; DB 13; Length 29;
XX Best local similarity: 76.2%; From: 130.0%;
XX Matches: 16; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;
XX QY 3 TCTGACGCTCAGAAAGATGAGG 23
XX    |||||
XX DB 2 TCTGACGCTCAGAAAGATGAGG 22
XX
XX RESULT 39
XX AAQ26169
XX ID AAQ26169 standard; DNA; 33 BP.
XX XX
XX AC AAQ26169;
XX XX
XX DT 28-SEP-2000 (first entry)
XX XX
XX DE PCR primer, StructBsp1201.
XX XX
XX KM Antigen presentation; vaccine; infectious disease; antibody; antibody;
XX KM molecular scaffold; immune response; farm animal; organism;
XX KM immunological; vaccine; infectious disease; antibody; PCR primer;
XX KM Jun leucine zipper; ss.
XX XX
XX OS Sindbis virus.
XX

```



CC to span larger or variable gaps, and a greater number of gaps, between  
CC DNA binding substrates. Sequences AA62334-357 represent PCR primers  
CC used in the course of the invention.

XX Sequence 15 PF: 4 A: 9 G: 14 T: 0 Other:

Query Match: 52.8%, Score 12.0, E: 22, Length 35;

Best Local Similarity: 83.3%, Fred. No. 1.1e-04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query 18 GAGGCGGAGAGAGATGAGG 23

DB 18 GATGCGGAGAGAGATGAGG 1

RESULT 14  
AA772379,  
ID AA772379 standard; DNA; 21 BP.

XX AA772379,  
AC AA772379,

XX 10 SEP-2001 (first entry)

XX Human biallelic marker upstream amplification primer; SEQ ID NO:6735

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotype; hybridization; identification; characterization;

XX method; single nucleotide polymorphism; SNP; PCR primer;

XX diagnosis; ss.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

Best Local Similarity: 76.2%, Fred. No. 1.2e-04;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 21 GAGGCGGAGAGATGAGG 25

DB 21 GATGCGGAGAGATGAGG 1

RESULT 15

ABN11989

XX ABN11989 standard; DNA; 25 BP.

XX ABN11989,

XX 29 MAY 2002 (first entry)

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotype; hybridization; identification; characterization;

XX method; single nucleotide polymorphism; SNP; PCR primer;

XX diagnosis; ss.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

Best Local Similarity: 76.2%, Fred. No. 1.2e-04;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 21 GAGGCGGAGAGATGAGG 25

DB 21 GATGCGGAGAGATGAGG 1

RESULT 15

ABN11989

XX ABN11989 standard; DNA; 25 BP.

XX ABN11989,

XX 29 MAY 2002 (first entry)

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotype; hybridization; identification; characterization;

XX method; single nucleotide polymorphism; SNP; PCR primer;

XX diagnosis; ss.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

[illegible][illegible]



08 FEB 2001; 2001WO-US04130.  
 08 FEB 2001; 2000US-0181099.  
 (GENA) GENAISCANCE PHARM INC.  
 Anastasio AB, Chow A, Dutton BR, Nandabalan K, Stephens JC,  
 WPI; 2001-522460/57.  
 Novel polynucleotide containing one of 11, Fc $\gamma$  R1, single nucleotide  
 polymorphisms in human interleukin-15 gene, and useful for treating  
 diseases affected by expression of function of interleukin-15 isogene

Example 1, Page 28, 29pp; English.  
 The present invention is a PCR primer useful for amplifying human  
 interleukin-15 (IL-15) gene fragment. IL-15 gene is located on  
 chromosome 4q11. The polymorphic variants of IL-15 genes are useful  
 for studying the expression and function of IL-15 and expressing  
 IL-15 protein for use in useful for screening for candidate drugs to  
 treat diseases related to IL-15 activity. Genotyping a haplotype  
 individual at the novel IL-15 polymorphic sites are useful for studying  
 polymorphism diversity, anthropological lineage, the significance of  
 diversity and lineage of the phenotypic level, paternity testing,  
 forensic applications and for identifying associated between IL-15  
 genetic variation and a trait such as level of drug response or  
 susceptibility to disease. Genotyping an individual between a genotype  
 of haplotype of IL-15 gene is useful for developing diagnostic tests and  
 therapeutic treatments for infectious, human immunodeficiency virus and  
 T-cell leukemia. The identification of an association between a clinical  
 response and a genotype or haplotype for haplotype part for the IL-15  
 gene may be the basis for designing a diagnostic method to determine  
 these individuals who will or will not respond to the treatment, or  
 alternatively, will respond at a lower level and thus may require more  
 treatment, i.e., a greater dose of a drug. The genotyping of haplotype  
 methods are also useful for developing drugs targeting IL-15. The  
 genotyping and haplotype methods are also useful in designing clinical  
 trials. IL-15 gene is useful for therapeutic purposes for treating  
 disorders affected by expression of function of novel IL-15 isogene and  
 also in gene therapy. Expression of IL-15 gene may be induced off  
 by transfecting a targeted cell, tissue or cell population of an  
 individual with a had expresses high levels of antineoplastic agent for  
 the isogene.

Sequence 21 BP; 5 A; 7 C; 6 G; 5 T; 0 other;  
 Quality Match 52.8%; Score 13.2; DB 22; Length 23;  
 Best local similarity 83.3%; Pred. No. 1e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0Y 8 GGGGCAAGATGACATTC 25  
 |||||  
 23 GCGCAGGAGATGACATTC 6

RESULT 30  
 AAS18161  
 ID AAS18161 standard; DNA; 24 BP.  
 AC AATATCT.  
 XX  
 XX  
 DT 26 MAR 2002 (first entry)  
 XX  
 DE CCRP Tag1B polymorphism detection PCR primer #1.  
 XX  
 XX Cardiac-related disease, CCRP polymorphism, coronary heart disease, SC,  
 XX cholesterol ester transfer protein, CCRP Tag 1 restriction sites;  
 XX cholesterol ester transfer protein, CCRP Tag 1 restriction sites;  
 XX coronary artery disease, coronary insufficiency, PCR primer, human,  
 XX Homo sapiens.

XX  
 PN W0200185999-A1.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PE 10-MAY-2001; 2001WO-US15013.  
 XX  
 PE 11-MAY-2000; 2000US-204467P.  
 XX  
 PA (TUFT) TUFTS COLLEGE.  
 XX  
 PA Ordway JM, Schaefer EJ,  
 XX  
 DR WPI; 2002-082902/11.  
 XX  
 PT Assessing risk for the development of cardiovascular disease in an  
 XX individual, comprises analyzing nucleic acid from the individual for  
 XX presence of TAP polymorphism of a secretory transmembrane  
 XX gene -  
 FS Claim 13; Page 67; 72pp; English.  
 XX  
 XX The invention relates to a method for assessing risk for development of  
 XX cardiovascular disease, comprising analyzing a nucleic acid from an  
 XX individual for the presence of TAP polymorphism of a secretory transmembrane  
 XX transfer protein, CCRP gene, and assessing the risk for development of  
 XX cardiovascular disease. The method involves determining whether the  
 XX individual is heterozygous for polymorphisms for at least two positions of  
 XX TAP polymorphism, whereby the absence of the polymorphisms correspond  
 XX with the frequency and phenotypic expression of coronary artery disease.  
 XX The invention also includes PCR primers used for amplification of a  
 XX suitable section of the first portion of the CCRP gene encompassing the  
 XX Tag1 restriction site of the first allele of the CCRP gene, the presence of  
 XX the Tag1 restriction site being indicative of the absence of the TAP  
 XX polymorphism. The cardiovascular diseases include myocardial infarction,  
 XX coronary artery disease, angina pectoris, coronary insufficiency and  
 XX coronary death. The sequence represented a PCR primer used in the method  
 XX of the invention.

Sequence 24 BP; 7 A; 7 C; 8 G; 2 T; 0 other;  
 Quality Match 52.8%; Score 13.2; DB 24; Length 24;  
 Best local similarity 83.3%; Pred. No. 1e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0Y 5 GAAATGCAAGATGACATTC 22  
 |||||  
 3 CTACCCAGAGAGAGAGAG 20

RESULT 31  
 AB197919/C  
 ID AB197919 standard; DNA; 31 BP.  
 AC AB197919;  
 XX  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Non-endogenous human GPR24 receptor mutagenic primer, SEQ ID NO: 340.  
 XX  
 XX Human G protein-coupled receptor; GPR24, non endogenous mutant;  
 XX constitutively activated GPR, amino acid, sequence, GPR24;  
 XX mutagenic primer; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX W0200177177-A2  
 XX  
 XX 18-NOV-2001.  
 XX  
 XX 05-APR-2001; 2001WO-US110998.  
 XX











XX WO200129213 A1.  
 XX 26 APR-2001.  
 XX 19-OCT-2001; JMW0104047  
 XX 19-OCT-1999; WO01010404  
 XX (WELL) WELLCOME TRUST LTD.  
 XX (MERR) MERCK & CO INC.  
 XX Todd JA, Twells SCJ, Moss CW, Bay E, Bay P, Coker CT, Hammond H,  
 XX Metker M.  
 XX WPI: 2001 30038/31.  
 XX  
 XX Isoforms of novel gene arising from alternative splicing and encoding  
 XX highly related proteins termed as SAPla and SAPlb, from the IDDM4 locus  
 XX on human chromosome 11p13, useful for treating IDDM and other diseases  
 XX  
 XX Claim 14; Page 08; 129pp; English.  
 XX  
 XX The invention relates to SAPL (SAPla) (separation-induced transcript 14)  
 XX associated protein-like) polypeptide, selected from SAPla polypeptide  
 XX isoforms and SAPL polypeptide isoforms. The SAPL polypeptides are  
 XX useful in gene therapy for treating and preventing insulin-dependent  
 XX diabetes mellitus (IDDM). Fragments of the SAPL cDNA are useful as primers  
 XX and probes. The SAPL polypeptides are useful in screening for a substance  
 XX e.g. a peptide or chemical compound, which interacts and/or binds with  
 XX them. Sequences ABR11984 represent PCR primers specific for the SAPL  
 XX cDNA.  
 XX  
 XX Sequence: 27 nt. 5' A, 3' C, 4 T, 0 other:  
 XX  
 XX Query Match: 54.4%; Score 13.6; EB 24; Length 25;  
 XX Best Local Similarity: 80.0%; Pred. No. 6, 7e-01;  
 XX Matches: 16; Conservative: 0; Mismatches: 4; Indels: 0; gaps: 0  
 XX  
 XX 1 CAAAGGCGGAGAGGATGATGCT 24  
 XX 2 CAAAGGCGGAGAGGATGATGCT 21  
 XX  
 XX RESULT 17  
 XX ABR11984  
 XX ID ABR11984 standard, DNA; 25 BP.  
 XX  
 XX AC ABR11984;  
 XX XX  
 XX DT 29 MAY 2002 (first entry)  
 XX XX  
 XX TF Human GWT-1 25-mer scanning SEQ ID NO:11975;  
 XX XX  
 XX Human genome-derived myelin type protein 17 GDMF-1; GDMF-1; heart;  
 XX muscle; cytosol; chromosome 22; gene therapy; vaccine; heart disease;  
 XX skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200192524 A2.  
 XX  
 XX 29 MAY-2001; 4001WO-US16981.  
 XX  
 XX 26 MAY-2001; 2000US-207456P.  
 XX 21 SEP-2001; 2000US-207456P.  
 XX 27 SEP-2001; 2000US-236592P.  
 XX 04-OCT-2001; 2000US-0024261  
 XX 30 JAN-2001; 2001WO-US00661.  
 XX 30 JAN-2001; 2001WO-US00662.  
 XX 30 JAN-2001; 2001WO-US00663.

XX 30-JAN-2001; 2001WO-US00664.  
 XX 30 JAN 2001; 2001WO-US00665.  
 XX 30-JAN-2001; 2001WO-US00666.  
 XX 30-JAN-2001; 2001WO-US00667.  
 XX 30 JAN 2001; 2001WO-US00668.  
 XX 30 JAN 2001; 2001WO-US00669.  
 XX 30-JAN-2001; 2001WO-US00670.  
 XX 05-FEB-2001; 2001US-26860P.  
 XX  
 XX (ABCM) ABCMICA INC.  
 XX  
 XX Gu Y, Ji Y, Fann CG, Haveli ER, Fark DR, Shen W, Chaudhry MB.  
 XX WPI: 2002 17946/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGMP-1  
 XX protein, or as specific hGMP-1 capture probes for  
 XX sulfate-enhanced laser desorption/ionization, recombinant human  
 XX myosin-like protein hGMP-1.  
 XX  
 XX Disclosure; SEQ ID 11975; 214pp; English.  
 XX  
 XX The present invention describes a human genome-derived myosin like  
 XX protein 1 (hGMP-1). The protein and polynucleotide sequences of  
 XX hGMP-1 can be used in gene therapy and vaccine production. The  
 XX hGMP-1 nucleic acids can be used as probes to detect, diagnostic  
 XX and quantify hGMP-1 nucleic acids in samples, as amplification  
 XX substrates, to provide initial substrates for the recombinant expression  
 XX of hGMP-1 protein variants having desired phenotypic improvements, and  
 XX for expressing the proteins. The hGMP-1 proteins or polypeptides may  
 XX be used as immunogens to raise antibodies that specifically recognize  
 XX hGMP-1 proteins, as standards in assays used to determine the  
 XX concentration and/or amount specificity of hGMP-1 proteins, as specific  
 XX biomolecule capture probes for sulfate-enhanced laser desorption  
 XX ionization, as therapeutic supplement in patients having specific  
 XX deficiency in hGMP-1 production, and in a gene therapy for  
 XX therapy. The following polynucleotide sequences are hGMP-1 may be used for  
 XX identifying a disorder associated with the expression of hGMP-1 in  
 XX particular heart and skeletal muscle disorders. hGMP-1 is involved in  
 XX the process of the present sequence reference to the sequence in the  
 XX screening of the hGMP-1 sequence in the exemplification of the present  
 XX invention.  
 XX N.B. The sequence data for this patent did not form part of the prior art  
 XX specification, but was obtained in electronic format directly from WPI  
 XX at [http://wipo.int/pub/published\\_pat\\_sequence](http://wipo.int/pub/published_pat_sequence).  
 XX  
 XX SEQ Sequence 25 BP; 7 A; 6 C; 11 G; 1 T; 0 other:  
 XX  
 XX Query Match: 54.4%; Score 13.6; EB 24; Length 25;  
 XX Best Local Similarity: 80.0%; Pred. No. 6, 7e-01;  
 XX Matches: 16; Conservative: 0; Mismatches: 4; Indels: 0; gaps: 0  
 XX  
 XX 1 TGGAGGCGGAGAGGATGATGCT 25  
 XX 2 TGGAGGCGGAGAGGATGATGCT 25  
 XX  
 XX RESULT 18  
 XX ABR11984  
 XX ID ABR11984 standard, DNA; 25 BP.  
 XX  
 XX AC ABR11984;  
 XX XX  
 XX DT 29 MAY 2002 (first entry)  
 XX XX  
 XX DE Human GDMF-1 25-mer scanning SEQ ID NO:11975;  
 XX XX  
 XX Human genome-derived myelin type protein 17 GDMF-1; GDMF-1; heart;  
 XX muscle; cytosol; chromosome 22; gene therapy; vaccine; heart disease;  
 XX skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 XX Homo sapiens.  
 XX

AC AAT60024;  
 XX  
 DE 18-NOV-1997 (first entry)  
 XX  
 DE Ikabos Gene functional inactivation PCR primer pool  
 XX  
 XX Thymocyte, thymus, spleen, liver, lymph node, thymic  
 XX Ikabos dehydrated cells, fibroblasts, lymphocytes, oligo,  
 XX polymerase chain reaction, ss  
 XX  
 OS Synthetic  
 XX  
 XX WC9709419 At.  
 XX  
 PD 13-MAR-1997  
 XX  
 XX 04-SEP-1997, 9800 001497  
 XX  
 XX 05-SEP-1997, 9800 003245  
 XX  
 PA (GENE ) GEN HOSPITAL CORP  
 XX  
 PI Georgopoulos K;  
 XX  
 DR WPI, 1997-192895/17.  
 XX  
 PT Metastatic melanoma, a highly aggressive cancer which is  
 XX known to regrow, and which is resistant to chemotherapy.  
 XX  
 PS Disclosure: Page 60; 49pp; English.  
 XX  
 CC A novel method has been provided for providing a proliferation  
 CC dehydrated cell. The method involves: (a) providing a normal living  
 CC an in-house-dehydrated cell; and (b) providing a proliferation-  
 CC dehydrated cell from the normal cell, wherein the proliferation-  
 CC especially useful in the treatment of cancer. The method  
 CC present evidence representing a first step in the development of  
 CC that treatment of the cancer is not a first step in the  
 CC leads to the functional inactivation.  
 XX  
 SC Sequence 24 BT, 7 A, 3 C, 1 G, 1 T, 1 other;  
 Query Match 55.2%, Score 23.9, 28.19, Length 24,  
 Best Local Similarity 99.2%, Prod No. 49707,  
 Matches 15; Conservation 0; Mismatches 0; Indels 0; Gaps 0;  
 1 GCTTCAAGGCTGAAATTT  
 5 GCTTCAAGGCTGAAATTT  
 RESULT 15  
 AA233393  
 ID AA233393 standard; DNA; 29 bp.  
 XX  
 AC AA233393;  
 XX  
 CT 29-FEB-2000 (first entry)  
 XX  
 DE Human secreted protein clone, HSP11, from CHO cells  
 XX  
 XX Human secreted protein; nutritional; cytokine; cell proliferation;  
 XX differentiation; immune stimulating; immune suppressive;  
 XX human fibroblasts; fibroblasts; tissue growth; cellular inhibition;  
 XX chemotaxis; chemotaxis; lymphocytes; cell growth; inhibition;  
 XX (1994) anti-inflammatory; adhesion; tumor invasion suppressor;  
 XX lymph inhibition; gene therapy; histiocytes; platelets;  
 XX  
 OS Synthetic  
 OS Homo sapiens  
 XX  
 XX WC9957132 At.

PD 11-NOV-1999.  
 XX  
 XX 07-MAY-1999, 9800-0509970.  
 XX  
 XX 07-MAY-1999, 9800-054564.  
 XX  
 XX 02-JUN-1999, 9800-0097645.  
 XX  
 XX 02-JUN-1999, 9800-0097645.  
 XX  
 XX 31-JUL-1999, 9800-0094935.  
 XX  
 XX 10-AUG-1999, 9800-0066660.  
 XX  
 XX 11-AUG-1999, 9800-0096068.  
 XX  
 XX 06-MAY-1999, 9800-0096068.  
 XX  
 PA (GENE ) GENETICS INST INC.  
 XX  
 XX  
 PI Jacobs R, McCoy JM, Lavallee EF, Collins-Panella JA, Evans G,  
 XX Moberg D, Treacy M, Agostino M, Steininger R, Bowman M,  
 XX Ehrlich Smith E, Wajsb A;  
 XX  
 XX WPI, 2000 052937/04.  
 XX  
 PT New polymers are created containing secreted human proteins, derived from  
 XX adult placenta, adult retina, fetal brain, fetal  
 XX  
 PS Disclosure: Page 472; 49pp; English.  
 XX  
 XX The present invention describes new human secreted proteins which were  
 XX isolated from adult placenta, adult retina, fetal brain, fetal kidney,  
 XX adult placenta, adult retina, adult kidney, adult placenta,  
 XX tissue, adult testis, and adult lymph node cDNA libraries. The human  
 XX secreted proteins, and the polynucleotides encoding them, are predicted  
 XX to have first-in-class activities which would make them suitable for  
 XX treatment, preventing or ameliorating medical conditions in humans and  
 XX animals. Expected activities include nutritional activity, cytokine  
 XX and cell proliferation/stimulation activity, immune stimulating  
 XX activity, and inhibition of suppressing activity, humoral immune regulation  
 XX activity, tissue growth activity, cell growth activity,  
 XX chemotaxis, chemotaxis activity, hematopoietic and immunologic  
 XX activity, leukocyte/lymphocyte activity, and differentially activity,  
 XX chemotaxis, chemotaxis activity, and differentially activity,  
 XX activity. The polynucleotides are also stated to be useful for gene  
 XX therapy. Methods to AA233393 which human secreted proteins, and  
 XX AA233393 to AA233393 represent human secreted proteins, given in the  
 XX present invention. The present invention represents a probe for a human  
 XX secreted protein gene, used in the exemplification of the present  
 XX invention.  
 XX  
 SC Sequence 29 BT, 3 A, 3 C, 1 G, 1 T, 1 other;  
 Query Match 55.2%, Score 17.9, 18.21, Length 29;  
 Best Local Similarity 92.3%; Prod No. 556-03;  
 Matches 15; Conservation 0; Mismatches 3; Indels 0; Gaps 0;  
 5 GCTTCAAGGCTGAAATTT  
 1 GCTTCAAGGCTGAAATTT  
 RESULT 16  
 AAP83320  
 ID AAP83320 standard; DNA; 29 bp.  
 XX  
 AC AAP83320;  
 XX  
 CT 03-JUL-2001 (first entry)  
 XX  
 DE Human cDNA specific primer 13644 5f.  
 XX  
 XX SAPL, STT4, STT4 associated proteins like; human; anti-diabetic;  
 XX insulin-induced transcription 4; SAPL, SAPL, gene therapy; insulin;  
 XX insulin dependent diabetes mellitus; PCR primer; ss.  
 XX  
 OS Synthetic  
 OS Homo sapiens  
 XX



CC or eliminating polynucleotide sequence and optimizing the sequence of  
CC overn-14n, using the biased codon usage in the yeast. The expression  
CC vector if the invention is useful for high yield production of overn-14n  
CC in the yeast of Pichia, preferably P. pastoris X33 or P. pastoris GS115,  
CC by transfecting the yeast with the expression vector, inducing protein  
CC expression with methanol, culturing the yeast in defined culture  
CC medium such as shake flask or fermenter, and purifying the protein  
CC from culture media. This polynucleotide sequence represents a PCR primer  
CC used to engineer the overn-14n gene of the invention.

CC Sequence 26 BP: 6 A; 7 C; 8 G; 5 T; 0 other;

Query Match 56.8%, Score 14, DB 24, Length 26;  
Best Local Similarity 77.3%, Pred. No. 4.4e+03;  
Matches 17, Conservation 0, Mismatches 5, Indels 0, Gaps 0;

CC 1 CATTGAGCTCCAGCAAGATGAG 22  
CC |||||  
ID AA171041 standard, (RNA), 20 BP.  
XX  
AC AA171041;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Reverse primer flanking chromosome 6 (pcc11) locus  
XX  
KM THW, tumour suppressor gene; human; breast cancer; melanoma;  
KM metastasis; diagnostic; dinucleotide repeat polymorphism;  
KM microsatellite DNA, chromosome 6, FCF primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN W0200190351-A1.  
XX  
PD 29-NOV-2001.  
XX  
PE 19-MAY-2001; 2001WO 0505627.  
XX  
FE 19-MAY 2000; 2000EP 0110692.  
XX  
EA (HOFF) HOFFMANN IA KOTHE & CO AG F.  
XX  
FI Hildebrandt T, Van Muijen G, Weidle U;  
XX  
DR WPI: 2002-10619//14.  
XX  
PT Detecting nucleotide acids in a sample for determining whether a cancer  
PT cell containing test sample from a human has potential for tumour  
PT progression, by using a THW primer, and identifying in human tumours  
PT cells as before.

CC Example 4: Page 22; 42pp; English.

CC The present sequence is the reverse primer of a primer pair (see  
CC also AA171040) that flanks the highly polymorphic dinucleotide  
CC repeat region of the pcc11 locus of human chromosome 6.  
CC Fluorescence labelled primers flanking D6S452, D6S1694 and D6S11  
CC were used in a PCR analysis to study the incidence of allelic loss  
CC at D6S452 of various cell lines and tumour biopsies. The human  
CC tumour suppressor gene THW (see AA171041) is located on chromosome  
CC 6q. THW shows downregulated expression in tumour cells. A process  
CC for determining whether a cancer cell-containing test sample has  
CC potential for tumour development, progression or metastasis  
CC involves determining the relative level of hybridisation of a  
CC probe comprising the THW gene to the sample. A test sample having  
CC no or low potential for tumour progression or metastasis will have  
CC a higher amount of the THW nucleotide acid than does a cancer cell  
CC sample which has a high tumour progression potential or a

CC metastatic potential.

XX  
XX Sequence 20 BP: 7 A; 4 C; 5 T; 0 other;

CC Query Match 77.3%, Score 13, DB 24, Length 20;  
CC Best Local Similarity 80.2%, Pred. No. 5.2e+03;  
CC Matches 15, Conservation 0, Mismatches 2, Indels 0, Gaps 0;

CC 2 TCGAGAGTCGAGAAAGAT 19  
CC |||||  
ID 4 TCGAGAGTCGAGAAAGAT 20  
XX  
DE Neomycin gene primer Neo1.  
XX  
KM Ikarcos, transgenic; transgenic animal; transgenic mouse; mice;  
KM immunocompetent; immune system disorder; nervous system disorder;  
KM animal model; lymphoma; neomycin; PCR; polynucleotide chain length;  
KM primer; ss.  
XX  
OS Synthetic.  
XX  
PN W09604372-A1.  
XX  
PD 15-FEB-1996.  
XX  
PE 28-JUL-1995; 95WO-US09345.  
XX  
FE 29-JUL-1994; 94US-0243300.  
XX  
EA (GHHO) GEN HOSTITAL CORP.  
XX  
FI Georgopoulos K;  
XX  
DR WPI: 1996-129389/13.  
XX  
PT Transgenic rodent having Ikarcos trans-gene (ref. mutated) is  
PT severely immunocompromised and can be used as model to determine  
PT effects of treatment for immune and nervous system disorders

CC Disclosure: Page 37; 102pp; English.

CC Transgenic mice were bred that had a targeted deletion of the DNA  
CC binding domain (exons 3 and 4) in the Ikarcos gene. The genotype  
CC of F1 and F2 mice was determined by PCR analysis of tail DNA using  
CC primers Neo1 (AA171075) and Neo2 (AA171074) from the Ikarcos gene. Ikarcos  
CC Ex3p (AA176073) and Ex4p (AA176074) from the Ikarcos gene. Ikarcos  
CC is heterozygous allele that have full length (5.5 kb) of Ikarcos  
CC gene that had no definitive T-cell progenitors, were bred.

CC Sequence 24 BP: 7 A; 6 C; 5 G; 2 T; 0 other;

Query Match 95.2%, Score 19, DB 17, Length 24;  
Best Local Similarity 96.4%, Pred. No. 5.4e+03;  
Matches 15, Conservation 0, Mismatches 2, Indels 0, Gaps 0;

CC 1 CGTCGAGCTCCAGCAAG 17  
CC |||||  
ID 5 CGTCGAGCTCCAGCAAG 21  
XX  
DE Neomycin gene primer Neo1.

XX  
KM Ikarcos, transgenic; transgenic animal; transgenic mouse; mice;  
KM immunocompetent; immune system disorder; nervous system disorder;  
KM animal model; lymphoma; neomycin; PCR; polynucleotide chain length;  
KM primer; ss.  
XX  
OS Synthetic.  
XX  
PN W09604372-A1.  
XX  
PD 15-FEB-1996.  
XX  
PE 28-JUL-1995; 95WO-US09345.  
XX  
FE 29-JUL-1994; 94US-0243300.  
XX  
EA (GHHO) GEN HOSTITAL CORP.  
XX  
FI Georgopoulos K;  
XX  
DR WPI: 1996-129389/13.  
XX  
PT Transgenic rodent having Ikarcos trans-gene (ref. mutated) is  
PT severely immunocompromised and can be used as model to determine  
PT effects of treatment for immune and nervous system disorders

CC Disclosure: Page 37; 102pp; English.

CC Transgenic mice were bred that had a targeted deletion of the DNA  
CC binding domain (exons 3 and 4) in the Ikarcos gene. The genotype  
CC of F1 and F2 mice was determined by PCR analysis of tail DNA using  
CC primers Neo1 (AA171075) and Neo2 (AA171074) from the Ikarcos gene. Ikarcos  
CC Ex3p (AA176073) and Ex4p (AA176074) from the Ikarcos gene. Ikarcos  
CC is heterozygous allele that have full length (5.5 kb) of Ikarcos  
CC gene that had no definitive T-cell progenitors, were bred.

CC Sequence 24 BP: 7 A; 6 C; 5 G; 2 T; 0 other;

Query Match 95.2%, Score 19, DB 17, Length 24;  
Best Local Similarity 96.4%, Pred. No. 5.4e+03;  
Matches 15, Conservation 0, Mismatches 2, Indels 0, Gaps 0;

CC 1 CGTCGAGCTCCAGCAAG 17  
CC |||||  
ID 5 CGTCGAGCTCCAGCAAG 21  
XX  
DE Neomycin gene primer Neo1.

XX  
KM Ikarcos, transgenic; transgenic animal; transgenic mouse; mice;  
KM immunocompetent; immune system disorder; nervous system disorder;  
KM animal model; lymphoma; neomycin; PCR; polynucleotide chain length;  
KM primer; ss.  
XX  
OS Synthetic.  
XX  
PN W09604372-A1.  
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PD 15-FEB-1996.  
XX  
PE 28-JUL-1995; 95WO-US09345.  
XX  
FE 29-JUL-1994; 94US-0243300.  
XX  
EA (GHHO) GEN HOSTITAL CORP.  
XX  
FI Georgopoulos K;  
XX  
DR WPI: 1996-129389/13.  
XX  
PT Transgenic rodent having Ikarcos trans-gene (ref. mutated) is  
PT severely immunocompromised and can be used as model to determine  
PT effects of treatment for immune and nervous system disorders

CC Disclosure: Page 37; 102pp; English.

CC Transgenic mice were bred that had a targeted deletion of the DNA  
CC binding domain (exons 3 and 4) in the Ikarcos gene. The genotype  
CC of F1 and F2 mice was determined by PCR analysis of tail DNA using  
CC primers Neo1 (AA171075) and Neo2 (AA171074) from the Ikarcos gene. Ikarcos  
CC Ex3p (AA176073) and Ex4p (AA176074) from the Ikarcos gene. Ikarcos  
CC is heterozygous allele that have full length (5.5 kb) of Ikarcos  
CC gene that had no definitive T-cell progenitors, were bred.







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FT      20
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FT      W0280152862 A1.
FT      26 JUL 2001.
FT      12 JAN 2001, 2001W0-0301020.
FT      19-JAN-2000, 2000US-0480765.
FT      (ISIS-) ISIS PHARM INC.
FT      Butler MM, McKay R, Menia BP, Wyatt JB;
FT      WPI; 2001 457510/49.
FT      Novel antisense compounds, particularly antisense oligonucleotides for
FT      inhibiting expression of glycogen synthase kinase 3 beta in cells and
FT      for diagnosing, treating neurological and insulin regulation disorders
FT      .
PS      Claim 3: Page 82, 106pp; English.
XX      CC The invention relates to antisense compounds targeted to
XX      CC nucleic acid encoding glycogen synthase kinase 3 beta (GSK3B)
XX      CC (also known as tau protein kinase 1 (TPK-1)).
XX      CC The antisense compound is useful for inhibiting the expression of
XX      CC glycogen synthase kinase 3 beta enzyme in cells of tissues and for
XX      CC treating diseases or conditions associated with the enzyme
XX      CC such as insulin regulation disorder, in particular diabetes and
XX      CC neurological disorder, e.g. Alzheimer's disease and bipolar
XX      CC illness. The antisense compound is also useful for diagnosing
XX      CC diseases associated with the expression of glycogen synthase kinase
XX      CC 3 beta and for prophylaxis e.g. to prevent or delay infection,
XX      CC inflammation or tumour formation and as a research reagent.
XX      CC The present sequence is an antisense compound targeted to
XX      CC human glycogen synthase kinase 3 beta mRNA.
XX      Sequence ID Ref: 1 A; 7 C; 1 G; 5 T; 0 other.
XX      Query Match 56.0%, Score 14, DB 20, Length 20,
XX      Best Local Similarity 100.0%, Prod. No. 452e+03;
XX      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX      QY 12 AAAAAATGAGGTC 25
XX      16 AAAAAATGAGGTC 3
XX      RESULT 5.
XX      AAD11520/c
XX      ID AAD11520 standard, RNA, 20 BP.
XX      AC AAD11520;
XX      DT 24 SEP-2001 (first entry)
XX      BE Human glycogen synthase kinase 3 beta antisense oligo IIS 117449.
XX      FW Antisense glycogen synthase kinase 3 beta, 20bp, diabetes, infection,
XX      FW insulin regulation disorder, neurological disorder, Alzheimer's disease,
XX      FW HIV infection, inflammation, tumour, fibroblast, TTP 1.
XX      KW tau protein kinase 1, human se
XX      OS Homo sapiens.
XX      Synthesis.
XX      OS Synthesis.

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XX      /note= "2' methoxyethyl (2' MOE) nucleotides"
XX      16..20
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "2' methoxyethyl (2' MOE) nucleotides"
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XX      /tag= d
XX      /mod_base= msc
XX      10
XX      /tag= e
XX      /mod_base= msc
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XX      modified_base
XX      15
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XX      19
XX      /tag= h
XX      /mod_base= msc
XX      W0280152862 A1.
XX      26-JUL-2001.
XX      12 JAN 2001, 2001W0-0301020.
XX      19-JAN-2000, 2000US-0480765.
XX      (ISIS-) ISIS PHARM INC.
XX      Butler MM, McKay R, Menia BP, Wyatt JB;
XX      WPI; 2001 457510/49.
XX      Novel antisense compounds, particularly antisense oligonucleotides for
XX      inhibiting expression of glycogen synthase kinase 3 beta in cells and
XX      for diagnosing, treating neurological and insulin regulation disorders
XX      .
PS      Claim 3: Page 82, 106pp; English.
XX      CC The invention relates to antisense compounds targeted to
XX      CC nucleic acid encoding glycogen synthase kinase 3 beta (GSK3B)
XX      CC (also known as tau protein kinase 1 (TPK-1)).
XX      CC The antisense compound is useful for inhibiting the expression of
XX      CC glycogen synthase kinase 3 beta enzyme in cells or tissues and for
XX      CC treating diseases or conditions associated with the enzyme
XX      CC such as insulin regulation disorder, in particular diabetes and
XX      CC neurological disorder, e.g. Alzheimer's disease and bipolar
XX      CC illness. The antisense compound is also useful for diagnosing
XX      CC diseases associated with the expression of glycogen synthase kinase
XX      CC 3 beta and for prophylaxis e.g. to prevent or delay infection,
XX      CC inflammation or tumour formation and as a research reagent.
XX      CC The present sequence is an antisense compound targeted to
XX      CC human glycogen synthase kinase 3 beta mRNA.
XX      Sequence ID Ref: 1 A; 5 C; 1 G; 1 T; 0 other.
XX      Query Match 56.0%, Score 14, DB 20, Length 20,
XX      Best Local Similarity 100.0%, Prod. No. 452e+03;
XX      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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```





[illegible]







C 375	11.4	45.6	28	19	AAV19834	Primer for human
C 376	11.4	45.6	29	19	AAV49802	Probe for coding s
C 377	11.4	45.6	29	21	AAAC0214	Human HPC2 cDNA ex
C 378	11.4	45.6	29	21	AAAC4161	Probe used to find
C 379	11.4	45.6	29	21	AAAC3801	Polymorphic fragme
C 380	11.4	45.6	29	21	AAAC02851	Polymorphic fragme
C 381	11.4	45.6	29	21	AAAC37522	Polymorphic fragme
C 382	11.4	45.6	29	21	AAAC41011	PCR primer for h
C 383	11.4	45.6	29	21	AAAC40516	Human cDNA clone B
C 384	11.4	45.6	30	24	AAAC40449	EF retention can
C 385	11.4	45.6	30	24	AAAC40399	EF retention can
C 386	11.4	45.6	30	24	AAAC40391	EF retention can
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C 388	11.4	45.6	30	24	AAAC40391	HSP nucleic acid 1
C 389	11.4	45.6	31	18	AAAC40391	Strand bound star
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C 393	11.4	45.6	32	20	AAAC40391	PCR primer used
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C 399	11.4	45.6	32	20	AAAC40391	PCR primer used
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C 406	11.4	45.6	32	20	AAAC40391	PCR primer used
C 407	11.4	45.6	32	20	AAAC40391	PCR primer used
C 408	11.4	45.6	32	20	AAAC40391	PCR primer used
C 409	11.4	45.6	32	20	AAAC40391	PCR primer used
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C 412	11.4	45.6	32	20	AAAC40391	PCR primer used
C 413	11.4	45.6	32	20	AAAC40391	PCR primer used
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C 415	11.4	45.6	32	20	AAAC40391	PCR primer used
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C 418	11.4	45.6	32	20	AAAC40391	PCR primer used
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JOURNAL Patent: US 5955300 A 01/27/99-1-44;  
 FEATURES Location/Qualifiers  
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 BASE COUNT 6 a 9 c 9 g 7 t  
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 30;  
 Best Local Similarity 70.8%; Pred. No. 3.5e+05;  
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 2 GTCCGAGGCCGAGAGATGAGGTC 25  
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 LOCUS  
 DEFINITION Sequence 7 from patent US 5955300.  
 ACCESSION AR075034  
 VERSION AR075034.1 GI:10091786  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 35)

AUTHORS Faure, F., Herceud, T., Huard, B. and Triebel, F.

TITLE Soluble polypeptide fragments of the LAG-3 protein: purification

METHOD Therapeutic composition, anti-idiotypic antibodies

JOURNAL Patent: US 5955300-A / 21-Sep-1999;

FEATURES Location/Qualifiers  
 source 1..35  
 BASE COUNT 10 a 9 c 9 g 7 t  
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 DEFINITION Sequence 7 from patent US 6143273.  
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 VERSION AR118498.1 GI:14100391  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 35)

AUTHORS Faure, F., Herceud, T., Huard, B. and Triebel, F.

TITLE Therapeutic composition containing antibodies to soluble

polypeptide fractions of LAG-3 protein

JOURNAL Patent: US 6143273 A 7-07-NOV-2000;

FEATURES Location/Qualifiers  
 source 1..35  
 BASE COUNT 10 a 9 c 9 g 7 t  
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EP / CGATTAAAGCCGAGAGATGAGGTC 30

Search completed: July 21, 2003, 14:55:16  
 CPU time: 266.1561 secs



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VERSION AP014609.1 GI:1371963  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Shin, H.-G., Shin, N.-K., Lee, I. and Kang, S.  
TITLE Tumor necrosis factor mRNA  
JOURNAL Patent: US 5773982 A 19 10-27-1999.  
FEATURES  
SOURCE 1..22  
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BASE COUNT 2 a 8 c 4 g 8 t  
ORIGIN

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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ACCESSION AX005915  
VERSION AX005915.1 GI:1392887  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Holling, R. and Reiter, A.  
TITLE Familial Mediterranean fever gene  
JOURNAL Patent: WO 9700594-A 6 25-Feb-1999;  
GERTHER, T. (FR), HELLIG, ROBERT (FR)  
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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ACCESSION AX418470  
VERSION AX418470.1 GI:1523162  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM Synthetic construct.

REFERENCE 1  
AUTHORS Rastelli, L., Shimkets, R.A., Zetshusen, R., Malyanar, T.M. and Padigam, M.  
TITLE Human polypeptides and polypeptides encoded thereby  
JOURNAL Patent: WO 970119 A 01 24-Jan-1997;  
Curagen Corporation (US)  
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION  
ACCESSION AX465571  
VERSION AX465571.1 GI:1499874  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Zetshusen, R., Padigam, M., Zyl, F.A., Zetshusen, R., Ganigoll, E.A., Rastelli, L., Burgess, C.E., Kalambou, F., Shalaby, E., Michra, V., Vernet, C.A., Szekeres, E.S., Zetshusen, R., Acedo, R., Liu, X., Gerlach, V.L., Ellerman, K., Smithson, G., Toyonaga, T., Padigam, M. and MacDougall, J.  
TITLE Proteins and nucleic acids encoding the same  
JOURNAL Patent: WO 9701468 A 09 21-Feb-1997;  
Curagen Corporation (US)  
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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23 GGCAGAGAGATGAG 8

RESULT 18  
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DEFINITION  
ACCESSION AP067153  
VERSION AP067153.1 GI:5998375  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 501)  
AUTHORS Evans, G.A. and Smith, M.W.  
TITLE Method for production of recombinant cytidine triphosphate of complex primary

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Hallig, P. and Perrot, A.  
 TITLE Familial Mediterranean fever gene  
 JOURNAL Patent WO 9900074 A12 43-FEB-1999  
 ORIGINION II (FR); HEILIG ROLAND (FR)  
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BASE COUNT 2 a 4 c 4 g 8 t  
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Query Match 51.2% Score 12.8; DB 6; Length 18;  
 Best Local Similarity 87.5%; Pred. No. 3.6e+05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

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 |||||  
 18 GAGCCCGAGAGATGA 3

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 DEFINITION Cytb gene from Patient W00337764.  
 ACCESSION AX020070  
 VERSION AX020070.1 GI:14043900  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Vogelstein, M. P. and David, G. J.  
 TITLE New members of the tyrosinase gene family  
 JOURNAL Patent WO 9407644 A 29 09-SEP-1994  
 ORIGINION W00337764 (DE); VILKAS INTERIMV INST BIOTECN  
 (DE); DAVID GUIDO JOSEPH FRANS (BE)  
 FEATURES  
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BASE COUNT 2 a 6 c 5 g 6 t  
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Query Match 51.2% Score 12.8; DB 6; Length 19;  
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 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

CY 3 GAGCCCGAGAGATG 20  
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 16 GAGCCCGAGAGATG 1

RESULT 31  
 AX020014/c  
 LOCUS AX020014 21 bp DNA linear PAT 07-SEP-2000  
 DEFINITION Sequence 28 from Patient W00337764.  
 ACCESSION AX020014  
 VERSION AX020014.1 GI:10043843  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Vogelstein, M. P. and David, G. J.  
 TITLE New members of the tyrosinase gene family  
 JOURNAL Patent WO 9407644 A 29 09-SEP-1994  
 ORIGINION W00337764 (DE); VILKAS INTERIMV INST BIOTECN  
 (DE); DAVID GUIDO JOSEPH FRANS (BE)  
 FEATURES  
 SOURCE Location/Qualifiers  
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BASE COUNT 5 a 5 c 5 g 6 t  
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Query Match 51.2% Score 12.8; DB 6; Length 21;  
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 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

CY 6 GAGCCCGAGAGATGA 21  
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 20 GAGCCCGAGAGATGA 5

RESULT 32  
 AX020070/c  
 LOCUS AX020070 21 bp DNA linear PAT 07 MAY 2000  
 DEFINITION Cytb gene from Patient W00337764.  
 ACCESSION AX020070  
 VERSION AX020070.1 GI:14043900  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Vogelstein, M. P. and David, G. J.  
 TITLE New members of the tyrosinase gene family  
 JOURNAL Patent WO 9407644 A 29 09-SEP-1994  
 ORIGINION W00337764 (DE); VILKAS INTERIMV INST BIOTECN  
 (DE); DAVID GUIDO JOSEPH FRANS (BE)  
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 SOURCE Location/Qualifiers  
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BASE COUNT 2 a 5 c 5 g 6 t  
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Query Match 51.2% Score 12.8; DB 6; Length 21;  
 Best Local Similarity 87.5%; Pred. No. 3.6e+05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

CY 6 GAGCCCGAGAGATGA 21  
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 20 GAGCCCGAGAGATGA 5

RESULT 33  
 AR014507/c  
 LOCUS AR014507 22 bp DNA linear PAT 07 SEP 1994  
 DEFINITION Sequence 55 from patent US 5773592.  
 ACCESSION AR014507  
 VERSION AR014507.1 GI:3371961  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Shih, H.-C., Shih, N.-R., Lee, J., and Kang, S.  
 TITLE Tumor necrosis factor mutants  
 JOURNAL Patent US 5773592 A 23 09-SEP-1993  
 ORIGINION US 5773592 A 23 09-SEP-1993  
 FEATURES  
 SOURCE Location/Qualifiers  
 1..22  
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BASE COUNT 2 a 8 c 4 g 8 t  
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Query Match 51.2% Score 12.8; DB 6; Length 22;  
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 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

CY 10 GAGCCCGAGAGATG 25  
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[illegible]

VERSION	AX370481	DB 61	Length 333
KEYWORDS	Synthetic construct.		
CORRE	Synthetic construct.		
CONTRAST	artificial sequences.		
REFERENCE	1 Schell, F., Tschopp, N., Eichenlaub, M., Tischer, A. and Leuchner, P. Molecular antigen arrays and vaccines Patent WO 99/05634 A 27 15 Nov 2001; Cyber Biotechnology AG (CH) ; Sebhel, Peter (CH) ; Immann, Nicolas (CH) ; Bachmann, Martin (CH) ; Tissot, Alain (CH) ; Gschwend, Franziska (CH)		
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	/db_xref="db:AX370481"		
	/note="Primer"		
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ORIGIN			
Query Match	99.98% Query 13 DB 61 Length 333		
Best Local Similarity	99.98% Ident. No. 2,999+051		
Matches	161 conservative 14 mismatches 14 gaps 14		
OY	5 GGAGCCGACGAAGAATGAACTT 25		
Ld	29 CTAGCAACGAGAAATGAAATG 9		
RESULT 28			
AX370481			
REFERENCE	AY370481	DB 61	PNA
SEQUENCE	Sequence 12 from Patent W9909049.		
ACCESSION	AX370481		
VERSION	AX370481.1		
KEYWORDS	G1:19857523		
SOURCE			
ORGANISM	Synthetic construct.		
	Synthetic construct.		
	artificial sequences.		
REFERENCE	1 Altevogt, P. and Fogel, J.M. Diagnostic and therapeutic methods based on the 12 different molecule for variant and endometrial tumors Patent. WO 02/49322 A 13 12 JAN 2002; Technische Universitaet Braunschweig Stiftung fuer Endokrinologische Diagnostik (DE) ; MOP-RESEARCH APPLICATIONS LTD. (UK) Location/Qualifiers		
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Matches	161 conservative 14 mismatches 14 gaps 14		
OY	2 GTCCGAGGCCGACGAAGAATGAG 22		
Ld	7 GCCCGACGAGATGAAAGATGAG 27		
RESULT 29			
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LOCUS	Sequence 12 from Patent W9909049.		
DEFINITION	AX006921		
ACCESSION	AX006921		
VERSION	AX006921.1		
KEYWORDS	G1:9928903		
SOURCE	unidentified.		
	unidentified.		
	unclassified.		

CY 6 GAGCCGAGAAAGATGAG 23  
 DB 18 GATCCGAAAGATGAG 1  
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 AX287759/c  
 LOCUS  
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 ACCESSION AX287759  
 VERSION AX287759.1 GI:17349375  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE Novel methods of constructing libraries of genetic packages that collectively display the members of a diverse family of polypeptides or proteins  
 JOURNAL Patent WO 01/79481 A 145 (5-0001-2001)  
 Dyax Corp. (US)  
 FEATURES  
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 LOCATION/Qualifiers  
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 /note="Synthetic primer"

BASE COUNT 6 a 6 c 4 g 6 t  
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 Query Match 52.0% Score 13; DB 6; Length 22;  
 Best Local Similarity 76.0% Freq. No. 2,9e+05;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 TCCGAGCCGAGAAAGATGAG 23  
 DB 21 TCCGTCGACAGTAATATGAG 1  
 RESULT 22  
 AX297939/c  
 LOCUS  
 DEFINITION Sequence 285 from Patent WO0179481  
 ACCESSION AX297939  
 VERSION AX297939.1 GI:17349487  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE Novel methods of constructing libraries of genetic packages that collectively display the members of a diverse family of polypeptides or proteins  
 JOURNAL Patent WO 01/79481 A 195 (5-0001-2001)  
 Dyax Corp. (US)  
 FEATURES  
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 LOCATION/Qualifiers  
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 /note="Synthetic primer"

BASE COUNT 6 a 6 c 4 g 6 t  
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 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 TCCGAGCCGAGAAAGATGAG 23  
 DB 21 TCCGTCGACAGTAATATGAG 1

RESULT 23  
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 LOCUS  
 DEFINITION Sequence 32 from Patent EP0955563  
 ACCESSION AX012431  
 VERSION AX012431.1 GI:3996470  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE Ena sequences encoding enzymes involved in production of isoprenoids  
 JOURNAL Patent EP 0955563 A 32 (9-NOV-1997)  
 HOFFMANN LA ROCHE (CH)  
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BASE COUNT 12 a 9 c 7 g 2 t  
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 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CTTTCATGTCGAAAGATGA 21  
 DB 6 CATGAAAGGCAAAAGAAAGA 26  
 RESULT 24  
 AX116559/c  
 LOCUS  
 DEFINITION Sequence 145 from Patent WO0179481  
 ACCESSION AX116559  
 VERSION AX116559.1 GI:14033501  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE Novel methods of constructing libraries of genetic packages that collectively display the members of a diverse family of polypeptides or proteins  
 JOURNAL Patent WO 01/79481 A 195 (5-0001-2001)  
 Dyax Corp. (US)  
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BASE COUNT 3 a 8 c 2 g 13 t  
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 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 11 CAGAAAGATGAG 23  
 DB 13 CAGAAAGATGAG 1  
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 DEFINITION Improved production of isoprenoid  
 ACCESSION ES1024  
 VERSION ES1024.1 GI:13023246  
 KEYWORDS  
 JP 2000050894-A/27

```

Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Evans, G.A. and Smith, M.W.
TITLE
Method for generation of sequence sampled maps of complex genomes
JOURNAL
Nature 364:179-184 (1998)
KEYWORDS
Location/Qualifiers
SOURCE
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/organism="unknown"

BASE COUNT
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Best Local Similarity 83.3% Score 13.2; DB 6; Length 19;
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Db

RESULT 17
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DEFINITION
AX280758
ACCESSION
AX280758.1 GI:16097731
VERSION
AX280758.1 GI:16097731
KEYWORDS
synthetic construct;
synthetic construct;
artificial sequences.
SOURCE
ORGANISM
human.
REFERENCE
1
AUTHORS
Lehmann-Hruska, K., Liaw, C.W. and Lin, J.L.
TITLE
Non-enzymous, conservatively activated known q protein coupled
receptors
JOURNAL
Patent: WO 0177172-A 181 18-OCT 2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source
1..31
location/Qualifiers
1..31
BASE COUNT
6 a 6 c 4 g 4 t

Query Match
Best Local Similarity 83.3% Score 13.2; DB 6; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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19 CCAGGCCAGAAAGATGA 18
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RESULT 18
AX280758
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Sequence 216 from Patent WO0177172.
DEFINITION
AX280758
ACCESSION
AX280758.1 GI:16097731
VERSION
AX280758.1 GI:16097731
KEYWORDS
synthetic construct;
synthetic construct;
artificial sequences.
SOURCE
ORGANISM
human.
REFERENCE
1
AUTHORS
Lehmann-Hruska, K., Liaw, C.W. and Lin, J.L.
TITLE
Non-enzymous, conservatively activated known q protein coupled
receptors
JOURNAL
Patent: WO 0177172-A 380 18-OCT 2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source
1..31
location/Qualifiers
1..31
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Query Match
Best Local Similarity 83.3% Score 13.2; DB 6; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

UY
4 CCAGGCCAGAAAGATGA 21
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RESULT 19
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LOCUS
Sequence 381 from Patent WO0177172.
DEFINITION
AX280758
ACCESSION
AX280758.1 GI:16098124
VERSION
AX280758.1 GI:16098124
KEYWORDS
synthetic construct;
synthetic construct;
artificial sequences.
SOURCE
ORGANISM
human.
REFERENCE
1
AUTHORS
Lehmann-Hruska, K., Liaw, C.W. and Lin, J.L.
TITLE
Non-enzymous, conservatively activated known q protein coupled
receptors
JOURNAL
Patent: WO 0177172-A 381 18-OCT 2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source
1..31
location/Qualifiers
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BASE COUNT
12 a 10 c 7 g 2 t

Query Match
Best Local Similarity 83.3% Score 13.2; DB 6; Length 41;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db

RESULT 20
AX282648
LOCUS
Sequence 121 from Patent WO0151480.
DEFINITION
AX282648
ACCESSION
AX282648.1 GI:15922314
VERSION
AX282648.1 GI:15922314
KEYWORDS
synthetic construct;
synthetic construct;
artificial sequences.
SOURCE
ORGANISM
human.
REFERENCE
1
AUTHORS
Choo, Y., Liaw, C.W. and Moore, M.T.
TITLE
Nucleic acid binding polypeptides characterized by flexible domains
connected nucleic acid binding codes
JOURNAL
Patent: WO 0153480 A 121 26-JUL 2001;
Genadag Limited (GB)
FEATURES
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/db_xref="taxon:12610"
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

UY
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RESULT 19
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LOCUS
Sequence 381 from Patent WO0177172.
DEFINITION
AX280758
ACCESSION
AX280758.1 GI:16098124
VERSION
AX280758.1 GI:16098124
KEYWORDS
synthetic construct;
synthetic construct;
artificial sequences.
SOURCE
ORGANISM
human.
REFERENCE
1
AUTHORS
Lehmann-Hruska, K., Liaw, C.W. and Lin, J.L.
TITLE
Non-enzymous, conservatively activated known q protein coupled
receptors
JOURNAL
Patent: WO 0177172-A 381 18-OCT 2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source
1..31
location/Qualifiers
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Query Match
Best Local Similarity 83.3% Score 13.2; DB 6; Length 41;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db

RESULT 20
AX282648
LOCUS
Sequence 121 from Patent WO0151480.
DEFINITION
AX282648
ACCESSION
AX282648.1 GI:15922314
VERSION
AX282648.1 GI:15922314
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synthetic construct;
synthetic construct;
artificial sequences.
SOURCE
ORGANISM
human.
REFERENCE
1
AUTHORS
Choo, Y., Liaw, C.W. and Moore, M.T.
TITLE
Nucleic acid binding polypeptides characterized by flexible domains
connected nucleic acid binding codes
JOURNAL
Patent: WO 0153480 A 121 26-JUL 2001;
Genadag Limited (GB)
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Best Local Similarity 83.3% Score 13.2; DB 6; Length 41;
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JOURNAL Patent: US 5608326-A 6 04 MAY 1997  
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 BASE COUNT 10 a 7 c 7 g 6 t  
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Query Match 53.6% Score 13.4) LR 6) Length 30  
 Best Local Similarity 53.6%, Fred No. 1.9e+05;  
 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528  
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 ACCESSION AR067333  
 VERSION AR067333.1 GI:1218555  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 30)  
 AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parry,C.B., Sullivan,D.M., Erb,L.J. and Lustig,R.D.  
 TITLE Method of identifying compounds which bind to the P-subunit receptor  
 JOURNAL Patent: US 5608326-A 6 04 MAY 1997;  
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BASE COUNT 10 a 7 c 7 g 6 t  
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 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528  
 DEFINITION Sequence 6 from patent US 5608326  
 ACCESSION AR067333  
 VERSION AR067333.1 GI:1218555  
 KEYWORDS  
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 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 30)  
 AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parry,C.B., Sullivan,D.M., Erb,L.J. and Lustig,R.D.  
 TITLE Method of identifying compounds which bind to the P-subunit receptor  
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LOCUS 136528  
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 ACCESSION AR067333  
 VERSION AR067333.1 GI:1218555  
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 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 30)  
 AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parry,C.B., Sullivan,D.M., Erb,L.J. and Lustig,R.D.  
 TITLE Method of identifying compounds which bind to the P-subunit receptor  
 JOURNAL Patent: US 5608326-A 6 04 MAY 1997;  
 LOCATION/Qualifiers  
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JOURNAL Patent: US 5608326-A 6 04 MAY 1997  
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Query Match 53.6% Score 13.4) LR 6) Length 30  
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LOCUS 136528  
 DEFINITION Sequence 6 from patent US 5608326  
 ACCESSION AR067333  
 VERSION AR067333.1 GI:1218555  
 KEYWORDS  
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 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 30)  
 AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parry,C.B., Sullivan,D.M., Erb,L.J. and Lustig,R.D.  
 TITLE Method of identifying compounds which bind to the P-subunit receptor  
 JOURNAL Patent: US 5608326-A 6 04 MAY 1997;  
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 Best Local Similarity 53.6%, Fred No. 1.9e+05;  
 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528  
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 ACCESSION AR067333  
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 KEYWORDS  
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 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 30)  
 AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parry,C.B., Sullivan,D.M., Erb,L.J. and Lustig,R.D.  
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 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528  
 DEFINITION Sequence 6 from patent US 5608326  
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 VERSION AR067333.1 GI:1218555  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 30)  
 AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parry,C.B., Sullivan,D.M., Erb,L.J. and Lustig,R.D.  
 TITLE Method of identifying compounds which bind to the P-subunit receptor  
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 /organism="unknown"

BASE COUNT 8 a 4 c 12 g 1 t 5 others  
 ORIGIN



PD 12 SEP 2000  
 PR 27 JAN 2000 (P 20001949)  
 PR 27 JAN 1999 (S 09/030 400)  
 PI NISA SHAW, GARY MALLINSON, NISA PATIL  
 PC G11151953, G11151954, G11151955  
 CC  
 FH Key Location/Qualifiers  
 FT source 1.031 /organism="unidentified"  
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BASE COUNT 8 a 5 c 8 g 9 t 1 others  
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Query Match 56.8% 81.0% 14.0% 19.6% length 31,  
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 24 CGAGCCGAGGAGGATAGCTG 4

DB 24 CGAGCCGAGGAGGATAGCTG 4

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 LOCUS  
 DEFINITION  
 AX316186  
 ACCESSION  
 AX316186.1 G1117999367  
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 KEYWORDS  
 SOURCE  
 ORGANISM  
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 SYNTHETIC RESEQUENCE  
 ARTIFICIAL SEQUENCES

REFERENCE  
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 AUTHOR  
 TITLE  
 JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 CYPTRAL

FEATURES  
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 /note="reverse primer"

BASE COUNT 7 a 4 c 6 g 3 t  
 ORIGIN

Query Match 55.0% 80.0% 13.0% 19.6% length 31,  
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CY 4 TCGAGCCGAGGAGGATAGCTG 19  
 |||||  
 4 TCGAGCCGAGGAGGATAGCTG 20

DB 4 TCGAGCCGAGGAGGATAGCTG 20

RESULT 5  
 AR125044  
 LOCUS  
 DEFINITION  
 AR125044  
 ACCESSION  
 AR125044.1 G1114110429  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 UNKNOWN  
 UNCLASSIFIED  
 REFERENCE  
 1 (bases 1 to 24)  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS

Query Match 55.0% 80.0% 13.0% 19.6% length 31,  
 Best Local Similarity 80.0% Prot No. 100000000,  
 Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0,

CY 4 TCGAGCCGAGGAGGATAGCTG 19  
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 4 TCGAGCCGAGGAGGATAGCTG 20

DB 4 TCGAGCCGAGGAGGATAGCTG 20

RESULT 6  
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 LOCUS  
 DEFINITION  
 AR055770  
 ACCESSION  
 AR055770.1 G115149533  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

REFERENCE  
 1  
 AUTHOR  
 TITLE  
 JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 CYPTRAL

FEATURES  
 SOURCE  
 1..33  
 /organism="Homo sapiens"  
 /db\_xref="taxid:9606"  
 /note="HBB00030"

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variation  
 1..12  
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variation  
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variation  
 1..12  
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CDS  
 28..233  
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 /translation="MT"

BASE COUNT 6 a 9 c 11 g 7 t  
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Query Match 55.0% 80.0% 13.0% 19.6% length 31,  
 Best Local Similarity 80.0% Prot No. 100000000,  
 Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0,

CY 1 CGAGCCGAGGAGGATAGCTG 17  
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DB 17 CGAGCCGAGGAGGATAGCTG 1

RESULT 7  
 AX119631

FEATURES  
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 1..24  
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BASE COUNT 7 a 9 c 6 g 2 t  
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Query Match 55.0% 80.0% 13.0% 19.6% length 24,  
 Best Local Similarity 80.0% Prot No. 100000000,  
 Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0,

CY 1 CGAGCCGAGGAGGATAGCTG 17  
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 17 CGAGCCGAGGAGGATAGCTG 1

DB 17 CGAGCCGAGGAGGATAGCTG 1

RESULT 7  
 AX119631

















## SUMMARIES

score greater than or equal to the score of the second highest ranked and is defined by analysis of the total score distribution.

(without alignments)  
2802.865 Million cell updates/sec

**Sequence:** I gttcctggaggtccacggaaccatgcataaacaggaaagt

Gapot 10.0 , Gapext 1.0

Total number of letters and syllables: 10,000

### Post-processing - Minimum Match

Minimum Match	0%
Maximum Match	100%
Listing First	100%
Summary	100%

Paraphrase

1: gb pat\*  
2: gb hcg\*  
3: gb int\*  
4: gb ex\*  
5: gb \_\*  
6: gb fat\*  
7: gb h\*  
8: gb fl\*  
9: gb pr\*  
10: gb ro\*  
11: gb sts\*  
12: gb sy\*  
13: gb unt\*  
14: gb vi\*  
15: em ba\*  
16: em fan\*  
17: em haw\*  
18: em h\*  
19: em mu\*  
20: em om\*  
21: em or\*  
22: em ov\*  
23: em pat\*  
24: em ph\*  
25: em pl\*  
26: em reg\*  
27: em sts\*  
28: em \_\*  
29: em vl\*  
30: em hcg hum\*  
31: em hcg inv\*  
32: em hcg other\*  
33: em hcg mus\*  
34: em hcg pin\*  
35: em hcg reg\*  
36: em hcg mam\*  
37: em hcg vit\*  
38: em sv\*  
39: em hcg hum\*  
40: em hcg \_\*  
41: em hcg other\*

Pred. No. is the number of regular growth by 0.0001

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	100.0	25	6	AX12827	AX12827 Sequence
2	14.1	98.4	21	6	AX14936	AX14936 Sequence
3	14.2	96.8	31	6	BD002615	BD002615 Sequence
4	13.8	95.2	20	6	AX116136	AX116136 Sequence
5	13.8	95.2	24	6	AR125044	AR125044 Sequence
6	13.6	95.2	33	9	AB055170	AB055170 Sequence
7	13.6	94.4	22	6	AX119631	AX119631 Sequence
8	13.6	94.4	30	6	AX107813	AX107813 Sequence
9	13.6	94.4	30	6	AX107824	AX107824 Sequence
10	13.4	93.6	27	6	AX116824	AX116824 Sequence
11	13.4	93.6	32	6	AX116824	AX116824 Sequence
12	13.4	93.6	30	6	AR070788	AR070788 Sequence
13	13.4	93.6	40	6	134577	134577 Sequence
14	13.4	93.6	30	6	136528	136528 Sequence
15	13.4	93.6	30	6	176284	176284 Sequence
16	13.2	93.6	32	6	AX061333	AX061333 Sequence
17	13.2	92.9	20	6	AX127020	AX127020 Sequence
18	13.2	92.9	31	6	AX090757	AX090757 Sequence
19	13.0	92.9	31	6	AX090758	AX090758 Sequence
20	12.9	92.9	35	6	AX090759	AX090759 Sequence
21	12.9	92.9	35	6	AX090760	AX090760 Sequence
22	12.9	92.9	35	6	AX090761	AX090761 Sequence
23	12.9	92.9	26	6	AX012431	AX012431 Sequence
24	12.9	92.9	26	6	AX116559	AX116559 Sequence
25	12.9	92.9	26	6	ES1024	ES1024 Sequence
26	12.9	92.9	33	6	AR146987	AR146987 Sequence
27	12.9	92.9	33	6	AX127163	AX127163 Sequence
28	12.9	92.9	33	6	AX176481	AX176481 Sequence
29	12.9	92.9	33	6	AX090762	AX090762 Sequence
30	12.9	92.9	19	6	AX116999	AX116999 Sequence
31	12.9	92.9	21	6	AX020014	AX020014 Sequence
32	12.9	92.9	22	6	AX014007	AX014007 Sequence
33	12.9	92.9	22	6	AR014009	AR014009 Sequence
34	12.9	92.9	26	6	AX014009	AX014009 Sequence
35	12.9	92.9	26	6	AX116910	AX116910 Sequence
36	12.9	92.9	26	6	AX116911	AX116911 Sequence
37	12.9	92.9	26	6	AX116912	AX116912 Sequence
38	12.9	92.9	30	6	AR067153	AR067153 Sequence
39	12.9	92.9	30	6	AR075034	AR075034 Sequence
40	12.9	92.9	30	6	AR116913	AR116913 Sequence
41	12.9	92.9	30	6	AR100057	AR100057 Sequence
42	12.9	92.9	28	6	ES1024	ES1024 Sequence
43	12.9	92.9	28	6	AX160474	AX160474 Sequence
44	12.9	92.9	28	6	176652	176652 Sequence
45	12.9	92.9	29	6	196651	196651 Sequence
46	12.9	92.9	35	6	ES16671	ES16671 Sequence
47	12.9	92.9	20	6	AX112196	AX112196 Sequence
48	12.9	92.9	21	6	AX112196	AX112196 Sequence
49	12.9	92.9	23	6	AX1144	AX1144 Sequence
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63	12.9	92.9	23	6	AX1144	AX1144 Sequence
64	12.9	92.9	23	6	AX1144	AX1144 Sequence
65	12.9	92.9	23	6	AX1144	AX1144 Sequence



## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

1 (bases 1 to 23)

Alonso, J.M., Leister, T.D., Barajas, P., Chen, H., Cheuk, F., Gadinab,

C., Jeske, A., Karnes, M., Kim, C.T., Parvett, H., Predits, L., Shinn, P.,

Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road,

La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

T-DNA.

## FEATURES

## source

Class: T-DNA tagged.

Location/Qualifiers

1..23

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_063270.52.90.x"

/clone\_lib "Arabidopsis thaliana T-DNA insertion lines"

/notes="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more T-DNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://salk.edu/thina\\_protocols.html](http://salk.edu/thina_protocols.html)"

## BASE COUNT

17 a 2 c 2 g 2 t

## ORIGIN

Query Match 40.7% Score 11; Dp 17; Length 23;

Best Local Similarity 73.7% Pred. No. 2e+06; 5; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 AATAGCTTACGACCAATA 27

DB 3 AATAGCTTACGACCAATA 21

Search completed: July 21, 2003, 15:47:50

Job time : 713.784 secs







RESULT 32  
 A2975330 12 bp 100% Linear GSS 27 APR 2001  
 LOCUS  
 EFFICIENT  
 ACCESSION  
 A2975330.1 GI:1384657  
 VERSION  
 KEYWORDS  
 ORGANISM  
 Mus musculus  
 house mouse  
 Eryavita, Metaxa, Chaitara, Stanilava, Vozelkara, Euclozevici,  
 Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.  
 1 (bases 1 to 29)  
 Burn, R., Ayoub, A., Parker, M., Pearson, T., Ewald, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmood, M., Memon, E., Pedersen, T., Pelly,  
 M., Rose, M., Ross, P., Seeger, P., Tadjy, A., von Bielefeld, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah  
 304, Biomedical Polymer Research Bldg., 20 S. 2030 E., SPO, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dumngenetics@utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plates: 6212 Low: 8 columns: 24  
 Seq primer: GTTGTAAAGAGAAAGGACAGT  
 Class: plasmid ends  
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 /sex="female"  
 /date="2001-04-11" strain: M11-2013, T1-resistant, F-  
 /note="Vector: pMT419V. Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Mouse  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/10kb-plasmid-inserts/). The DNA  
 was hydrolytically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adapter oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapter DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMT419V (pMT419V-10000). A copy number  
 inducible derivative of plasmid p1. The vector was ligated  
 with adapter oligonucleotides. The insert adapters and  
 purified. The sheared, adapter mouse DNA was annealed to  
 adapter vector DNA, and transformed into  
 chemically competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

RESULT 33  
 A2975330 12 bp 100% Linear GSS 27 APR 2001  
 LOCUS  
 EFFICIENT  
 ACCESSION  
 A2975330.1 GI:1384657  
 VERSION  
 KEYWORDS  
 ORGANISM  
 Mus musculus  
 house mouse  
 Eryavita, Metaxa, Chaitara, Stanilava, Vozelkara, Euclozevici,  
 Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.  
 1 (bases 1 to 32)  
 Burn, R., Ayoub, A., Parker, M., Pearson, T., Ewald, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmood, M., Memon, E., Pedersen, T., Pelly,  
 M., Rose, M., Ross, P., Seeger, P., Tadjy, A., von Bielefeld, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah  
 304, Biomedical Polymer Research Bldg., 20 S. 2030 E., SPO, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dumngenetics@utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plates: 6212 Low: 8 columns: 20  
 Seq primer: GTTGTAAAGAGAAAGGACAGT  
 Class: plasmid ends  
 High quality sequence: step: 30.  
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 source  
 1..32  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
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 /mol\_type="genomic DNA"  
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 musculus C57BL/6J (female) was obtained from the Mouse  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/10kb-plasmid-inserts/). The DNA  
 was hydrolytically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adapter oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapter DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMT419V (pMT419V-10000). A copy number  
 inducible derivative of plasmid p1. The vector was ligated  
 with adapter oligonucleotides. The insert adapters and  
 purified. The sheared, adapter mouse DNA was annealed to  
 adapter vector DNA, and transformed into  
 chemically competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."









BASE COUNT	6	3	8	0	7	9	1	2
ORIGIN								
Query Match			43 0%		Score 11.6;	DB 17;	length 34;	
Fast Local Similarity			77 8%		Pred. No. 1.2e+06;			
Matches	14;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps
QY	4	TTAGGATATACCTAACGA	21					
Db	31	TTAGGACGACCTTAAGAA	14					

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BASE COUNT      3   a       b   c       d   e   f   g   h   i   j   k   l   m   n   o   p   q   r   s   t   u   v   w   x   y   z
ORIGIN
Query Match          43.0%;    Score 11.6;    DB 17;    Length 24;
Best Local Similarity 77.8%;    Refid No. 1.2e+06;
Matches      14;    Conservative     0;    Mismatches      4;    Indels        0;    Gaps         0;
QY              9    AATACTAACGACCAAT 26
                ||| |||| | |||| | ||
Db             34  AAAAAGTATGACACAT 17

```

be found at: <http://olgrad.sak.edu/edu/gradinfo.htm>

Adapted from "The Gold Standard," by John Galsworthy, copyright © 1908 by H. K. Mulford.

and collected for impaction testing."

















1345 base pair. Cell strain X110-Gold, T resistant, F<sup>+</sup> (Mitsunobu, 1999). Purified genomic DNA from M. musculus C57BL/6J (Jax) was obtained from the Jackson Laboratory mouse DNA repository (<http://www.jax.org/resources/documents/index/>). The DNA was hydrolytically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end ligated with 14 DNA fragments of 14 polynucleotide kinase (Adipath) digested DNA. The ligated to the blunt ends in high molar excess. The adapter-1 DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The DNA was prepared from a derivative of pMD19 (G117211418) (ATCC20221), a copy-number inducible derivative of plasmid p1. The vector was ligated with adapter complementary to the insert adapters and purified. The sheared, adapter-mouse DNA was annealed to a 14 bp end of the DNA, and a restriction site (XbaI) was introduced. The DNA was digested with XbaI and selected for ampicillin resistance."

## BASE COUNT

12 A 9 C 4 G 7 T

## ORIGIN

Query Match 49.8% Score 13.41 DB 12 Length 32  
Best local similarity 49.8% Ident 100%  
Matches 17 Conserved 0 Mismatches 0 Indels 0 Gaps 0

2 CCTGACATACCTACACACAA 24  
|||||  
1 CCTAGCCTACACACACAA 23

## Dn

2 CCTGACATACCTACACACAA 24

## RESULT 3

BH853496/c

## LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

Accession

Version

Keywords

Source

1345 base pair. Cell strain X110-Gold, T resistant, F<sup>+</sup> (Mitsunobu, 1999). Purified genomic DNA from M. musculus C57BL/6J (Jax) was obtained from the Jackson Laboratory mouse DNA repository (<http://www.jax.org/resources/documents/index/>). The DNA was hydrolytically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end ligated with 14 DNA fragments of 14 polynucleotide kinase (Adipath) digested DNA. The ligated to the blunt ends in high molar excess. The adapter-1 DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The DNA was prepared from a derivative of pMD19 (G117211418) (ATCC20221), a copy-number inducible derivative of plasmid p1. The vector was ligated with adapter complementary to the insert adapters and purified. The sheared, adapter-mouse DNA was annealed to a 14 bp end of the DNA, and a restriction site (XbaI) was introduced. The DNA was digested with XbaI and selected for ampicillin resistance."

## BASE COUNT

12 A 9 C 4 G 7 T

## ORIGIN

Query Match 49.8% Score 13.41 DB 12 Length 32  
Best local similarity 49.8% Ident 100%  
Matches 17 Conserved 0 Mismatches 0 Indels 0 Gaps 0

2 CCTGACATACCTACACACAA 24  
|||||  
1 CCTAGCCTACACACACAA 23

## Dn

2 CCTGACATACCTACACACAA 24

## RESULT 4

BH853496/c

## LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

Accession

Version

Keywords

1345 base pair. Cell strain X110-Gold, T resistant, F<sup>+</sup> (Mitsunobu, 1999). Purified genomic DNA from M. musculus C57BL/6J (Jax) was obtained from the Jackson Laboratory mouse DNA repository (<http://www.jax.org/resources/documents/index/>). The DNA was hydrolytically sheared by repeated passage through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end ligated with 14 DNA fragments of 14 polynucleotide kinase (Adipath) digested DNA. The ligated to the blunt ends in high molar excess. The adapter-1 DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The DNA was prepared from a derivative of pMD19 (G117211418) (ATCC20221), a copy-number inducible derivative of plasmid p1. The vector was ligated with adapter complementary to the insert adapters and purified. The sheared, adapter-mouse DNA was annealed to a 14 bp end of the DNA, and a restriction site (XbaI) was introduced. The DNA was digested with XbaI and selected for ampicillin resistance."

## BASE COUNT

12 A 9 C 4 G 7 T

## ORIGIN

Query Match 49.8% Score 13.41 DB 12 Length 32  
Best local similarity 49.8% Ident 100%  
Matches 17 Conserved 0 Mismatches 0 Indels 0 Gaps 0

2 CCTGACATACCTACACACAA 24  
|||||  
1 CCTAGCCTACACACACAA 23

## Dn

2 CCTGACATACCTACACACAA 24

## RESULT 5

BH853496/c

## LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

Accession

Version

Keywords

956	6.4	11.1	25	17	TALSHUUP
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960	8.4	11.1	27	17	A2447654
961	8.4	11.1	27	17	A2785632
962	8.4	11.1	27	17	A2811577
963	8.4	11.1	27	17	A2814740
964	8.4	11.1	27	17	A2837068
965	8.4	11.1	27	17	BH740817
966	8.4	11.1	27	17	TALSHUUP
967	8.4	11.1	27	17	TALSHUUP
968	8.4	11.1	28	9	AA006876
969	8.4	11.1	28	9	AA007809
970	8.4	11.1	28	9	A1040239
971	8.4	11.1	28	9	A1648648
972	8.4	11.1	28	9	A1681705
973	8.4	11.1	28	14	PA0084
974	8.4	11.1	28	17	AA005035
975	8.4	11.1	28	17	A2100041
976	8.4	11.1	28	17	A2105026
977	8.4	11.1	28	17	A2145871
978	8.4	11.1	28	17	A2346727
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980	8.4	11.1	28	17	A2785734
981	8.4	11.1	28	17	A2785734
982	8.4	11.1	28	17	BH790823
983	8.4	11.1	28	17	BH852579
984	8.4	11.1	28	17	BH856531
985	8.4	11.1	29	9	AU058420
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987	8.4	11.1	29	17	A2344707
988	8.4	11.1	29	17	A2345451
989	8.4	11.1	29	17	A2345748
990	8.4	11.1	29	17	A2785732
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992	8.4	11.1	29	17	BH866445
993	8.4	11.1	29	17	TALSHUUP
994	8.4	11.1	30	9	ALSA8443
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996	8.4	11.1	30	9	AU057897
997	8.4	11.1	30	9	AU057897
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999	8.4	11.1	30	9	AU057897
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1001	8.4	11.1	30	9	AU057897
1002	8.4	11.1	30	9	AU057897
1003	8.4	11.1	30	9	AU057897
1004	8.4	11.1	30	9	AU057897
1005	8.4	11.1	30	9	AU057897
1006	8.4	11.1	30	9	AU057897
1007	8.4	11.1	30	9	AU057897
1008	8.4	11.1	30	9	AU057897
1009	8.4	11.1	30	9	AU057897
1010	8.4	11.1	30	9	AU057897
1011	8.4	11.1	30	9	AU057897
1012	8.4	11.1	30	9	AU057897
1013	8.4	11.1	30	9	AU057897
1014	8.4	11.1	30	9	AU057897
1015	8.4	11.1	30	9	AU057897
1016	8.4	11.1	30	9	AU057897
1017	8.4	11.1	30	9	AU057897
1018	8.4	11.1	30	9	AU057897
1019	8.4	11.1	30	9	AU057897
1020	8.4	11.1	30	9	AU057897
1021	8.4	11.1	30	9	AU057897
1022	8.4	11.1	30	9	AU057897
1023	8.4	11.1	30	9	AU057897
1024	8.4	11.1	30	9	AU057897
1025	8.4	11.1	30	9	AU057897
1026	8.4	11.1	30	9	AU057897
1027	8.4	11.1	30	9	AU057897
1028	8.4	11.1	30	9	AU057897
1029	8.4	11.1	30		

## ALIGNMENTS

[illegible]

```

10000 R. Tenny, Pineda 5, 41, 13, 11111, 06 92007, TNA
Tel: 868 483 4100 x1762
Fax: 868 554 6170
Email: ckersnell@du
This is single pass sequence recovered from the left border of
TNA. This sequence lies within an inverted repeat of Arabidopsis
Class: TNA tagged.
FEATURE
source
1..35
1..10:inverted_repeats
/organism="Arabidopsis thaliana"
/strain="Columbia-0"
/db_xref="taxon:3702"
/clone="SALK_064024"
/clone_lib="Arabidopsis thaliana TNA insertion lines"
/seq_type="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TNA insertion
elements. The resultant fragment (for each line) was
directly sequenced to determine the insertion sequence at
the site of insertion. Details of the procedure used can
be found at http://signal.salk.edu/pubs/genomic.html"

```

[illegible]



[illegible]









80	10.6	19.1	2.1	17	TA126500	AL464901 T. Brucei	0	152	10.2	27.9	35	17	PH464154	PH464154
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C 82	10.6	19.1	2.4	17	A2740000	A2740000 IM064702	0	155	10.6	27.9	35	17	A2740000	A2740000
C 83	10.6	19.1	2.5	9	AL464770	AL464770 SB16111 Y	0	156	10.6	27.9	35	17	AL464770	AL464770
C 84	10.6	19.1	2.5	9	AL464770	AL464770 SB16111 Y	0	157	10.6	27.9	35	17	AL464770	AL464770
C 85	10.6	19.1	2.5	9	AL464770	AL464770 SB16111 Y	0	158	10.6	27.9	35	17	AL464770	AL464770
C 86	10.6	19.1	2.5	14	D18740	D18740 MS058445	0	159	10.6	27.9	35	17	D18740	D18740
C 87	10.6	19.1	2.5	14	D18740	D18740 MS058445	0	160	10.6	27.9	35	17	D18740	D18740
C 88	10.6	19.1	2.5	17	A2740000	A2740000 IM064702	0	161	10.6	27.9	35	17	A2740000	A2740000
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C 92	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	165	10.6	27.9	35	17	TA126500	TA126500
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C 95	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	168	10.6	27.9	35	17	TA126500	TA126500
C 96	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	169	10.6	27.9	35	17	TA126500	TA126500
C 97	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	170	10.6	27.9	35	17	TA126500	TA126500
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C 99	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	172	10.6	27.9	35	17	TA126500	TA126500
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C 102	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	175	10.6	27.9	35	17	TA126500	TA126500
C 103	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	176	10.6	27.9	35	17	TA126500	TA126500
C 104	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	177	10.6	27.9	35	17	TA126500	TA126500
C 105	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	178	10.6	27.9	35	17	TA126500	TA126500
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C 107	10.6	19.1	2.5	17	TA126500	TA126500 IM064702	0	180	10.6	27.9	35	17	TA126500	TA1





RESULT 32  
US-10-269-152 4/2  
Sequence 4: Affiliation: US/1007993  
Publication No. US2003010390A1  
GENERAL INFORMATION:  
AFFILIANT: University of Illinois  
TITLE OF INVENTION: Therapeutic Agent  
FILE REFERENCE: UNIPALISPT  
CURRENT AFFILIATION NUMBER: 1007993  
CURRENT FILING DATE: 2002-10-01  
PRIORITY FILING DATE: 1998-04-09  
PRIORITY FILING DATE: 1998-04-09  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-269-152 1

Query Match 47.4% Score 12.8; DB 15; Length 19;  
Best Local Similarity 87.0% Freq No 2 40794;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2Y 3 CTGAGCAATACCTAAC 18  
DB 16 CTGAGCAATACCTAAC 1

RESULT 33  
US-10-269-557-89/0  
Sequence 89: Application US/10269557  
Publication No. US2003010390A1  
GENERAL INFORMATION:  
APPLICANT: Micronix, Inc.  
TITLE OF INVENTION: WHAT DOES GENES AND PROTEINS FROM  
TITLE OF INVENTION: MICROSERIES MEMBRANES/STRESS CHANNEL MEMBRANES AND A MEMBRANE  
FILE REFERENCE: 870193411  
CURRENT AFFILIATION NUMBER: US/1007993  
CURRENT FILING DATE: 2002-10-01  
PRIORITY FILING DATE: 1998-04-09  
PRIORITY FILING DATE: 1998-04-09  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 88  
LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Filed 1991 by Micronix Corporation for the purpose of  
OTHER INFORMATION: gene and its function Artificially designed Human  
OTHER INFORMATION: expression plasmids  
US-10-269-557-88

Query Match 47.4% Score 12.8; DB 15; Length 19;  
Best Local Similarity 87.0% Freq No 2 40794;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2Y 3 CTGAGCAATACCTAAC 18  
DB 16 CTGAGCAATACCTAAC 1

RESULT 34  
US-10-269-079-41/2  
Sequence 41: Affiliation: US/1007993  
Publication No. US2003010390A1  
GENERAL INFORMATION:  
APPLICANT: Micronix, Inc.  
TITLE OF INVENTION: Fusion Proteins  
FILE REFERENCE: 06746 004-US-03

CURRENT AFFILIATION NUMBER: US/1007993  
CURRENT FILING DATE: 2002-10-01  
PRIORITY FILING DATE: 1998-04-09  
PRIORITY FILING DATE: 1998-04-09  
PRIORITY FILING DATE: 2001-11-13  
PRIORITY FILING DATE: 2001-11-13  
PRIORITY FILING DATE: 2001-04-12  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 41  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Cited in the patent US 6,158,117  
US-10-118-079-41

Query Match 47.4% Score 12.8; DB 15; Length 19;  
Best Local Similarity 87.0% Freq No 2 40794;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2Y 3 CTGAGCAATACCTAAC 18  
DB 16 CTGAGCAATACCTAAC 1

RESULT 35  
US-10-098-2538-26991  
Sequence 26991: Application US/100982638  
Publication No. US2003010390A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT AFFILIATION NUMBER: 100982638  
CURRENT FILING DATE: 2001-01-08  
PRIORITY FILING DATE: 2001-03-16  
PRIORITY FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 26991  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-098-2538-26991

Query Match 47.4% Score 12.8; DB 15; Length 25;  
Best Local Similarity 70.8% Freq No 2 40794;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

2Y 1 CTGAGCAATACCTAAC 24  
DB 1 CTGAGCAATACCTAAC 24

RESULT 36  
US-10-269-557-89/0  
Sequence 89: Application US/10269557  
Publication No. US2003010390A1  
GENERAL INFORMATION:  
APPLICANT: Miltman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT AFFILIATION NUMBER: 100982638  
CURRENT FILING DATE: 2001-01-08  
PRIORITY FILING DATE: 2001-03-16  
PRIORITY FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 26992  
LENGTH: 25  
TYPE: DNA

ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Primer  
 US 09-771-943-141

Query Match 48.1% Score 12.8; DB 1% Length 19  
 Best Local Similarity 86.2% Pred. No. 2.4e+04  
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 5 GAGCAATACCTAACCAAAA 25  
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 Db 21 GAGCAATATATCAACAAA 1

RESULT 28  
 US 09-812-777-8/c  
 Sequence 6, Application US/09812777  
 Publication No. US20020115827A1  
 GENERAL INFORMATION:  
 APPLICANT: KIM, KEY SUN  
 TITLE OF INVENTION: A METHOD FOR TISSUE STABILIZATION  
 FILE REFERENCE: US 09/0981277  
 CURRENT APPLICATION NUMBER: US/09/812-777  
 PRIOR FILING DATE: 2001-09-14  
 PRIOR APPLICATION NUMBER: KR 00-63506  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: Patent In Ver. 2.1  
 SEQ ID NO 8  
 LENGTH: 19  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Primer  
 US 09 812 777-8

Query Match 47.4% Score 12.8; DB 1% Length 19  
 Best Local Similarity 87.5% Pred. No. 2.4e+04  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 3 CTGAGCAATACCTAAC 18  
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 Db 16 CTGAGCAATACCTAAC 1

RESULT 29  
 US 09-847-172-16/c  
 Sequence 6, Application US/09847172  
 Publication No. US2003006973A1  
 GENERAL INFORMATION:  
 APPLICANT: CENTER FOR HEALTH AND SCIENCE UNIVERSITY  
 APPLICANT: VANSEBARE, ARTHUR A  
 TITLE OF INVENTION: PEPTIDE-INDUCED M-M CELLULAR REPLY & MANIPULATION OF ANTIGEN-SPRO  
 FILE REFERENCE: 899-58137  
 CURRENT APPLICATION NUMBER: US/09/847,172  
 PRIOR FILING DATE: 2001-07-01  
 PRIOR APPLICATION NUMBER: US 00/200,342  
 PRIOR FILING DATE: 2000-05-01  
 PRIOR APPLICATION NUMBER: US 09/153,586  
 PRIOR FILING DATE: 1998-09-16  
 PRIOR APPLICATION NUMBER: US 60/064,555  
 PRIOR FILING DATE: 1997-10-10  
 PRIOR APPLICATION NUMBER: US 00/064,502  
 PRIOR FILING DATE: 1997-09-16  
 NUMBER OF SEQ ID NOS: 44  
 SOFTWARE: Patent In Version 3.1  
 SEQ ID NO 36  
 LENGTH: 19  
 TYPE: DNA  
 ORGANISM: Artificial Sequence

FEATURE:  
 OTHER INFORMATION: PCR primer  
 US 09 847-172-36

Query Match 47.4% Score 12.8; DB 1% Length 19  
 Best Local Similarity 87.5% Pred. No. 2.4e+04  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 3 CTGAGCAATACCTAAC 18  
 |||||  
 Db 16 CTGAGCAATACCTAAC 1

RESULT 30  
 US-10-260-351-4/c  
 Sequence 4, Application US/10260351  
 Publication No. US2004006753A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Bristol  
 TITLE OF INVENTION: Therapeutic Agent  
 FILE REFERENCE: US/09/150,150  
 CURRENT APPLICATION NUMBER: US/10/260,351  
 PRIOR FILING DATE: 2004-10-01  
 PRIOR APPLICATION NUMBER: GB000721.1  
 PRIOR FILING DATE: 1998-04-09  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: Patent In Version 3.1  
 SEQ ID NO 4  
 LENGTH: 19  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-260-351-4

Query Match 47.4% Score 12.8; DB 1% Length 19  
 Best Local Similarity 87.5% Pred. No. 2.4e+04  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 3 CTGAGCAATACCTAAC 18  
 |||||  
 Db 16 CTGAGCAATACCTAAC 1

RESULT 31  
 US-10-216-705-7/c  
 Sequence 7, Application US/10216705  
 Publication No. US20030096973A1  
 GENERAL INFORMATION:  
 APPLICANT: Meristem Therapeutics, S.A.  
 TITLE OF INVENTION: Selective and targeted proteome modulation by 1,4-bis, Mo  
 FILE REFERENCE: 1149-3 DIV  
 CURRENT APPLICATION NUMBER: US/10/216,705  
 PRIOR FILING DATE: 2002-08-09  
 PRIOR APPLICATION NUMBER: US 09/331,347  
 PRIOR FILING DATE: 1999-08-17  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: Patent In Version 3.1  
 SEQ ID NO 7  
 LENGTH: 19  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: T7 Primase primer  
 US-10-216-705-7

Query Match 47.4% Score 12.8; DB 1% Length 19  
 Best Local Similarity 87.5% Pred. No. 2.4e+04  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 3 CTGAGCAATACCTAAC 18  
 |||||  
 Db 16 CTGAGCAATACCTAAC 1

Query Match 48 187 Score 133 DB 15 Length 25  
 Best Local Similarity 76.0%, Field No. 26104  
 Matches 16 Conserved 0 Mismatches 5 Indels 0

Cy 5 GAGCAATACCTTACGACACCA 23  
 Db 22 GTGAGTAATACCTTACGACCA 1

RESULT 23

US-10-098-263B-78252

Sequence 23633, Application US/09/098-263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human MHC Class II

FILE REFERENCE: 331817

CURRENT APPLICATION NUMBER: US/09/098-263B

CURRENT FILING DATE: 2003-02-08

PRIOR APPLICATION NUMBER: 68/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 13066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 29739

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-098-263B-78252

Query Match 48 187 Score 133 DB 15 Length 25  
 Best Local Similarity 76.0%, Field No. 26104  
 Matches 16 Conserved 0 Mismatches 5 Indels 0

Cy 5 GAGCAATACCTTACGACACCA 25  
 Db 25 GAGCAATACCTTACGACACCA 5

RESULT 24

US-10-098-263B-78252

Sequence 76222, Application US/09/098-263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 311817

CURRENT APPLICATION NUMBER: US/09/098-263B

CURRENT FILING DATE: 2003-02-08

PRIOR APPLICATION NUMBER: 68/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 13066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 78252

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-098-263B-78252

Query Match 48 187 Score 133 DB 15 Length 25  
 Best Local Similarity 76.0%, Field No. 26104  
 Matches 16 Conserved 0 Mismatches 5 Indels 0

Cy 1 TCTGAGCAATACCTTACGACCA 21  
 Db 4 TCTGAGCAATACCTTACGACCA 24

RESULT 25

US-10-098-263B-78252

Sequence 124511, Application US/09/098-263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 331817

CURRENT APPLICATION NUMBER: US/09/098-263B

CURRENT FILING DATE: 2003-02-08

PRIOR APPLICATION NUMBER: 68/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 13066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 124511

LENGTH: 25

TYPE: DNA

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 331817

CURRENT APPLICATION NUMBER: US/09/098-263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 68/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 13066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 124511

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-098-263B-124511

Query Match 48 187 Score 133 DB 15 Length 25  
 Best Local Similarity 76.0%, Field No. 26104  
 Matches 16 Conserved 0 Mismatches 5 Indels 0

Cy 5 GAGCAATACCTTACGACACCA 25  
 Db 24 GTGAGTAATACCTTACGACCA 4

RESULT 26

US-09-864-636A-2383

Sequence 23633, Application US/09/864-636A  
 Publication No. US20030104376A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 331817

CURRENT APPLICATION NUMBER: US/09/864-636A

CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 2640

SOFTWARE: Patent version 3.0

SEQ ID NO 2383

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US 09 864 636A 2383

Query Match 48 187 Score 133 DB 15 Length 28  
 Best Local Similarity 76.0%, Field No. 2383  
 Matches 16 Conserved 0 Mismatches 5 Indels 0

Cy 3 GTGAGTAATACCTTACGACCA 23  
 Db 8 GTGAGTAATACCTTACGACCA 28

RESULT 27

US-09-771-933-141C

Sequence 141, Application US/09/771-933  
 Publication No. US2003010387A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Computer-assisted Means for Assessing Lifestyle Risk

FILE REFERENCE: 620-130

CURRENT APPLICATION NUMBER: US/09/771-933

CURRENT FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 405

SOFTWARE: Patent version 2.1

SEQ ID NO 141

LENGTH: 30

TYPE: DNA

RESULT 18  
 US-10-151-902-9  
 / Sequence: 9, Affiliation: US/1519352  
 / File Reference: 319  
 / CURRENT APPLICATION NUMBER: US/09/081,576  
 / CURRENT FILING DATE: 2002-09-24  
 / PRIORITY FILING DATE: 1998-05-19  
 / PRIORITY FILING DATE: 1997-09-23  
 / PRIORITY FILING DATE: 1995-05-19  
 / SOFTWARE: Patent In Ver. 2.0  
 / SEQ ID NO: 9  
 / LENGTH: 35  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 US-10-151-902-9

Query Match 48.1% Score 13.2 DB 15 Length 35  
 Best Local Similarity At 18, Pred No 17 and 1  
 Matches 15: Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 9 AATGCTAATGCAAT 26  
 DB 12 AATGCTAATGCAAT 29

RESULT 19  
 US-09-754-853A-916-7  
 / Sequence: 819, Affiliation: US/097483A  
 / Publication No: US20030104410A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Hauser, Brian M.  
 / APPLICANT: Patrelli, Laurence D.  
 / APPLICANT: Parsons, Jeremy D.  
 / APPLICANT: Wang, Ming Li  
 / TITLE OF INVENTION: Multiple Anti-Medical And Other Molecules Associated With  
 / FILE REFERENCE: 38-1045810B  
 / CURRENT APPLICATION NUMBER: US/09/081,576  
 / CURRENT FILING DATE: 2001-01-05  
 / PRIORITY FILING DATE: 2000-01-07  
 / PRIORITY FILING DATE: 2000-01-07  
 / NUMBER OF SEQ ID NOS: 1119  
 / SEQ ID NO: 819  
 / LENGTH: 25  
 / TYPE: DNA  
 / ORGANISM: Glycine max  
 / FEATURE:  
 / OTHER INFORMATION: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25  
 US-09-754-853A-919

Query Match 48.1% Score 13.2 DB 15 Length 25  
 Best Local Similarity At 18, Pred No 17 and 1  
 Matches 16: Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 3 CTGACATACCTACGACAA 23  
 DB 25 CTGACATACCTACGACAA 5

RESULT 20  
 US-10-218-112-161-7  
 / Sequence: 1613, Affiliation: US/1615112  
 / Publication No: US2003082596A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Michael Miltmann

TITLE OF INVENTION: Method of Genetic Analysis of Proteins  
 / FILE REFERENCE: 319  
 / CURRENT APPLICATION NUMBER: US/09/081,576  
 / CURRENT FILING DATE: 2002-09-24  
 / PRIORITY FILING DATE: 1998-05-19  
 / PRIORITY FILING DATE: 1997-09-23  
 / PRIORITY FILING DATE: 1995-05-19  
 / SOFTWARE: Patent In Ver. 2.0  
 / SEQ ID NO: 1613  
 / LENGTH: 25  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthesis of oligonucleotide  
 US-10-218-112-1613

Query Match 48.1% Score 13.2 DB 15 Length 25  
 Best Local Similarity At 18, Pred No 17 and 1  
 Matches 15: Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 4 TGACATACCTACGACAA 24  
 DB 25 TGACATACCTACGACAA 5

RESULT 21  
 US-10-098-263B-16473/C  
 / Sequence: 16473, Affiliation: US/098263B  
 / Publication No: US20030104410A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Miltman, Michael  
 / APPLICANT: Human Microarray  
 / TITLE OF INVENTION: Human Microarray  
 / FILE REFERENCE: 3118-1  
 / CURRENT APPLICATION NUMBER: US/10/098,263B  
 / CURRENT FILING DATE: 2003-01-08  
 / PRIORITY FILING DATE: 2001-03-16  
 / PRIORITY FILING DATE: 2001-03-16  
 / SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 / SEQ ID NO: 16473  
 / LENGTH: 25  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 US-10-098-263B-16473

Query Match 48.1% Score 13.2 DB 15 Length 25  
 Best Local Similarity At 18, Pred No 17 and 1  
 Matches 15: Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 5 GAGCATACCTACGACAA 25  
 DB 21 GAGCATACCTACGACAA 1

RESULT 22  
 US-10-098-263B-17109/C  
 / Sequence: 17109, Affiliation: US/098263B  
 / Publication No: US20030104410A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Miltman, Michael  
 / APPLICANT: Human Microarray  
 / TITLE OF INVENTION: Human Microarray  
 / FILE REFERENCE: 3118-1  
 / CURRENT APPLICATION NUMBER: US/10/098,263B  
 / CURRENT FILING DATE: 2003-01-08  
 / PRIORITY FILING DATE: 2001-03-16  
 / PRIORITY FILING DATE: 2001-03-16  
 / SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 / SEQ ID NO: 17109  
 / LENGTH: 25  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 US-10-098-263B-17109

Query Match 48.1% Score 13.2 DB 15 Length 25  
 Best Local Similarity At 18, Pred No 17 and 1  
 Matches 15: Conservative 0, Mismatches 0, Indels 0, Gaps 0

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO: 19564  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-098-263B-19564

Query Match: 48.9% Score 13.47 DB 15; Length 25;  
 Best Local Similarity: 69.2% Prod. No. 1.7e+04;  
 Matches: 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 3 CTGAGCAATACCTAACGACAAATA 25  
 DB 25 CTGAGCAATACCTAACGACAAATA 3

RESULT 14  
 US-10-098-263B-19564  
 Sequence: 19564, Application US/098263B  
 Publication No. US20030007841A1  
 GENERAL INFORMATION:  
 APPLICANT: Mettler, Michael  
 TITLE OF INVENTION: Human Milk  
 FILE REFERENCE: 31484  
 CURRENT FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 2001-03-16  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 131065  
 SOFTWARE: Mismatch Index Sequence Listing Generator V 1.1  
 SEQ ID NO: 19564  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-098-263B-19564

Query Match: 48.9% Score 13.47 DB 15; Length 25;  
 Best Local Similarity: 69.2% Prod. No. 1.7e+04;  
 Matches: 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 5 GAGCATACCTAACGAC 22  
 DB 25 GAGCATACCTAACGAC 8

RESULT 15  
 US-09-894-799 17  
 Sequence: 17, Application US/09894799  
 Publication No. US20030007841A1  
 GENERAL INFORMATION:  
 APPLICANT: Mettler, Michael  
 TITLE OF INVENTION: Human Milk  
 FILE REFERENCE: 31484  
 CURRENT FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 2001-03-16  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 131065  
 SOFTWARE: Mismatch Index Sequence Listing Generator V 1.1  
 SEQ ID NO: 17  
 LENGTH: 30  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:  
 OTHER INFORMATION: oligonucleotide  
 US-09-894-799-17

Query Match: 48.9% Score 13.47 DB 15; Length 30;  
 Best Local Similarity: 69.2% Prod. No. 1.7e+04;  
 Matches: 15, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 1 FCGTAGCAATACCTAAC 18  
 DB 9 FCGTAGCAATACCTAAC 26

RESULT 16  
 US-10-095-906-179  
 Sequence: 179, Application US/10095906  
 Publication No. US20030054371A1  
 GENERAL INFORMATION:  
 APPLICANT: Ying, Vincent  
 APPLICANT: Wu, Paul  
 APPLICANT: Gray, Gary S.  
 TITLE OF INVENTION: POLYMERASE CHAIN REACTION IN THE  
 PRESENCE OF A POLYMERASE INHIBITOR  
 FILE REFERENCE: GNN 534302  
 CURRENT FILING DATE: 2002-02-27  
 PRIOR APPLICATION NUMBER: 2002-02-27  
 PRIOR FILING DATE: 1999-03-25  
 PRIOR FILING DATE: 1999-03-25  
 PRIOR FILING DATE: 1999-03-25  
 PRIOR FILING DATE: 1999-03-25  
 PRIOR FILING DATE: 1999-03-25  
 NUMBER OF SEQ ID NOS: 545  
 SOFTWARE: FASTASeq 1.1 Windows Version 4.0  
 SEQ ID NO: 179  
 LENGTH: 30  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-095-906-179

Query Match: 48.9% Score 13.47 DB 15; Length 30;  
 Best Local Similarity: 69.2% Prod. No. 1.7e+04;  
 Matches: 18, Conservative 0, Mismatches 8, Indels 0, Gaps 0

CY 1 CTGAGCAATACCTAAC 27  
 DB 1 CCGCAGCAATGCTACGAC 26

RESULT 17  
 US-10-156-306-3091  
 Sequence: 3091, Application US/10156306  
 Publication No. US2003011901A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 APPLICANT: Meszinger, James  
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Nucleic Acid  
 FILE REFERENCE: 31484  
 CURRENT FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 2001-03-16  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 8013  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 3091  
 LENGTH: 31  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 US-10-156-306-3091

Query Match: 48.9% Score 13.47 DB 15; Length 31;  
 Best Local Similarity: 69.2% Prod. No. 1.7e+04;  
 Matches: 18, Conservative 0, Mismatches 8, Indels 0, Gaps 0

CY 2 CTGAGCAATACCTAAC 27  
 DB 5 CTGAGCAATACCTAAC 30



Matches 18, Conservative 0, Mismatches 7, Indels 0, Gaps 0,

CY 1 TGTGACATACCTAAAGAACAA 23  
 |||||  
 TB 7 TGTGACATACCTAAAGAACAA 31

## RESULT 9

US-10-098-263B-18746

Sequence 18746, Application US/10098263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: US/09/761,142

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 14066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 3514

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-4514

Query Match 50.4%, Score 13.6, DB 15, Length 25,  
 Best Local Similarity 80.0%, Pred. No. 1,1e+04;

Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0;

CY 1 TGTGACATACCTAAAGAACAA 20  
 |||||  
 TB 23 TGTGACATACCTAAAGAACAA 4

US-10-098-263B-18746

Sequence 18746, Application US/10098263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: US/09/761,142

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 14066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 18746

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-18746

Query Match 50.4%, Score 13.6, DB 15, Length 25,  
 Best Local Similarity 80.0%, Pred. No. 1,1e+04;

Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0;

CY 4 TGTGACATACCTAAAGAACAA 23  
 |||||  
 TB 1 TGTGACATACCTAAAGAACAA 20

US-10-098-263B-19564/C

Sequence 19564, Application US/10098263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: US/09/761,142

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 14066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 19564

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-18746

APPLICANT: Kamdar, Kim  
 TITLE OF INVENTION: Synthetic Amino Acids and Peptides from Phosphonate and Sulfonate that Mimic  
 FILE REFERENCE: 31133B  
 CURRENT APPLICATION NUMBER: US/09/761,142  
 CURRENT FILING DATE: 2003-01-08  
 PRIOR APPLICATION NUMBER: US/09/761,142  
 PRIOR FILING DATE: 2001-01-16  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificially Synthesized Peptides

US-10-108-605-1

Query Match 50.4%, Score 13.6, DB 15, Length 27,  
 Best Local Similarity 80.0%, Pred. No. 1,1e+04;

Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0;

CY 4 TGTGACATACCTAAAGAACAA 23  
 |||||  
 TB 23 TGTGACATACCTAAAGAACAA 3

US-10-215-112-5782/C

Sequence 5782, Application US/10215112  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Michael Miltman

TITLE OF INVENTION: Method of Genetic Analysis of Proteins

FILE REFERENCE: 3113

CURRENT APPLICATION NUMBER: US/10/215,112

CURRENT FILING DATE: 2003-08-08

NUMBER OF SEQ ID NOS: 14936

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5782

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-5782

Query Match 49.6%, Score 13.4, DB 15, Length 25,  
 Best Local Similarity 73.9%, Pred. No. 1,1e+04;

Matches 17, Conservative 0, Mismatches 6, Indels 0, Gaps 0;

CY 2 CTTGACATACCTAAAGAACAA 24  
 |||||  
 TB 25 CTTGACATACCTAAAGAACAA 3

US-10-098-263B-19564/C

Sequence 19564, Application US/10098263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: US/09/761,142

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 14066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 19564

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-19564/C

Query Match 49.6%, Score 13.4, DB 15, Length 25,  
 Best Local Similarity 73.9%, Pred. No. 1,1e+04;

Matches 17, Conservative 0, Mismatches 6, Indels 0, Gaps 0;

CY 2 CTTGACATACCTAAAGAACAA 24  
 |||||  
 TB 25 CTTGACATACCTAAAGAACAA 3

US-10-098-263B-19564/C

Sequence 19564, Application US/10098263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: US/09/761,142

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 14066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 19564

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-19564/C

Query Match 49.6%, Score 13.4, DB 15, Length 25,  
 Best Local Similarity 73.9%, Pred. No. 1,1e+04;

Matches 17, Conservative 0, Mismatches 6, Indels 0, Gaps 0;

CY 2 CTTGACATACCTAAAGAACAA 24  
 |||||  
 TB 25 CTTGACATACCTAAAGAACAA 3

US-10-098-263B-19564/C

Sequence 19564, Application US/10098263B  
 Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: US/09/761,142

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 14066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 19564

LENGTH: 25

TYPE: DNA

```

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,272
FILING DATE: 22 Jan 2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/96/064
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Adelle
REGISTRATION NUMBER: 309-8512
REFERENCE/DEPT NUMBER: 309-8512
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO. 1:
US-09-766-272.248

```

```

Query Match: 55.0%, Score 15, DB 15, Length 35
Best Local Similarity: 79.1%, Pval: No. 2,9e+03,
Matches: 18, Conservative: 0, Mismatches: 1, Indels: 0, Gaps: 0

```

```

CY 5 GAGGATATAGCTTACGACAAATA 27
DB 34 GACCAATACCAAGGAAACAAATA 12

```

```

RESULT 5
US-10-098-263B-86994/C
Sequence: 86994, Application: US/09/92263B
Publication No.: US2003010410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT AFFILIATION NUMBER: HST/09/92,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 86994
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-86994

```

```

Query Match: 51.0%, Score 14, DB 15, Length 25
Best Local Similarity: 100.0%, Pval: No. 7.4e+03,
Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

```

```

CY 14 CTACGACAAATA 27
DB 15 CTACGACAAATA 2

```

```

RESULT 6
US-10-099-263B-11978/C
Sequence: 11978, Application: US/09/9263B
Publication No.: US2003010410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT AFFILIATION NUMBER: HST/09/92,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759

```

```

PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 118078
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-118078

```

```

Query Match: 51.0%, Score 14, DB 15, Length 25
Best Local Similarity: 77.0%, Pval: No. 7.4e+03,
Matches: 14, Conservative: 0, Mismatches: 1, Indels: 0, Gaps: 0

```

```

CY 1 TCCGACAAATAGCTTACGACAA 22
DB 24 TCCGACAAATAGCTTACGAC 3

```

```

RESULT 7
US-10-098-263B-41030/C
Sequence: 41030, Application: US/09/92263B
Publication No.: US2003010410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT AFFILIATION NUMBER: HST/09/92,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 41030
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-41030

```

```

Query Match: 51.1%, Score 13.8, DB 15, Length 25
Best Local Similarity: 73.0%, Pval: No. 9.1e+03,
Matches: 19, Conservative: 0, Mismatches: 7, Indels: 0, Gaps: 0

```

```

CY 2 CTACGACAAATAGCTTACGACAA 26
DB 25 CATAGTAGGACCTACGACATAT 1

```

```

RESULT 8
US-09-918-036-15
Sequence: 15, Application: US/09/918036
Publication No.: US2003010410A1
GENERAL INFORMATION:
APPLICANT: MADURA, Kiran
TITLE OF INVENTION: METHOD FOR ANALYZING DNA FOR THE PRESENCE OF A SPECIFIC SEQUENCE
FILE REFERENCE: 066/165
CURRENT AFFILIATION NUMBER: US/09/918,036
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/200,171
PRIOR FILING DATE: 1997-06-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 15
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Oligonucleotide (15-mer) primer for amplification of a specific DNA sequence
OTHER INFORMATION: 5' to 3' direction
US-09-918-036-15

```

```

Query Match: 51.1%, Score 13.8, DB 12, Length 32
Best Local Similarity: 72.0%, Pval: No. 9.4e+03,

```

```

C 966 10.2 37.8 25 15 US-10-098-2638-44086 Sequence 83466, A
C 967 10.2 37.8 25 15 US-10-098-2638-44032 Sequence 44032, A
C 968 10.2 37.8 25 15 US-10-098-2638-82416 Sequence 82416, A
C 969 10.2 37.8 25 15 US-10-098-2638-90147 Sequence 90147, A
C 970 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 971 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 972 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 973 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 974 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 975 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 976 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 977 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 978 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 979 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 980 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 981 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 982 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 983 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 984 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 985 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 986 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 987 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 988 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 989 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 990 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 991 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 992 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 993 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 994 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 995 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 996 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 997 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 998 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A
C 999 10.2 37.8 25 15 US-10-098-2638-10147 Sequence 10147, A

```

## ALIGNMENTS

```

RESULT 1
US-10-098-2638-115419/C
Sequence 115419, Affiliation: Human Microarray
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mitteran, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 2638
PRIORITY FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 115419
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2638-115419

```

```

Query Match 5/48, Score 15.5, DB 15, Length 25,
Best Local Similarity 91.93, Pct 15.5, 0.03
Matches 18, Conservative 0, Mismatches 4, Indels 0, Gaps 0
4 CTAGCATACCTAGGACAA 25
25 TGAATATACCTAGGACAA 4

```

```

RESULT 2
US-10-098-2638-115420/C
Sequence 115420, Affiliation: Human Microarray
Publication No. US20030104410A1

```

```

GENERAL INFORMATION:
APPLICANT: Mitteran, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 2638
PRIORITY FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 115420
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2638-115420

```

## RESULT 3

```

US-10-098-2638-115420/C
Sequence 115420, Affiliation: Human Microarray
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mitteran, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 2638
PRIORITY FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,759
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 115420
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2638-115420

```

## RESULT 4

```

US-10-098-2638-115420/C
Sequence 115420, Affiliation: Human Microarray
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 2638
PRIORITY FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/276,759
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 115420
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2638-115420

```

```

Query Match 5/48, Score 15.5, DB 15, Length 25,
Best Local Similarity 91.93, Pct 15.5, 0.03
Matches 18, Conservative 0, Mismatches 4, Indels 0, Gaps 0
3 CTAGCATACCTAGGACAA 25
25 TGAATATACCTAGGACAA 3

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44M
COMPILED BY: VLSI 446/33
OPERATING SYSTEM: MS-DOS 6.2

```



[illegible]



[illegible]









1 APPLICANT: Chung, Ming Yi  
 2 APPLICANT: Zeng, Hui Yi  
 3 TITLE OF INVENTION: Gene Sequence for Spinothalamic Ataxia  
 4 Patent No. 6834183  
 5 TITLE OF INVENTION: TYPE 1 and Method for Diagnosis  
 6 NUMBER OF SEQUENCES: 85  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESS: P.O. Box 581415  
 9 CITY: Minneapolis  
 10 STATE: MN  
 11 COUNTRY: USA  
 12 ZIP: 55458-1415  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 COMPUTER: IBM PC compatible  
 16 OPERATING SYSTEM: PC DOS/MS DOS  
 17 SOFTWARE: FASTA/BLAST Release #1.0, Version #1.0  
 18 CURRENT APPLICATION DATA:  
 19 APPLICATION NUMBER: US/09/000,803B  
 20 FILING DATE: 29 JUN 1994  
 21 CLASSIFICATION: 415  
 22 ATTORNEY/AGENT INFORMATION:  
 23 NAME: McCormack, Myra H.  
 24 REGISTRATION NUMBER: 36,602  
 25 REFERENCE/AGENT INFORMATION:  
 26 TELEPHONE: 612-305-1217  
 27 TELEFAX: 612-305-1224  
 28 INFORMATION FOR SEQ ID NO: 21:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 22 base pairs  
 31 TYPE: nucleic acid  
 32 STRANDEDNESS: single  
 33 TOPOLOGY: linear  
 34 MOLECULE TYPE: DNA  
 35 US 09-890-363-4  
 36  
 37 Query Match: 45.8% Score 12.41 DB 1 Length 28:  
 38 Best Local Similarity 82.0% Prod. No. 32e+03  
 39 Matches 16, Conservation 0, Mismatches 6, Indels 0, Gaps 0  
 40  
 41 RESULT 39  
 42 US 09-890-363-4  
 43 Sequence 6, Application US/09/000,803B  
 44 Patent No. 6194638  
 45 GENERAL INFORMATION:  
 46 APPLICANT: Bhargava, Karanpal  
 47 APPLICANT: Faltys, Patricia Lynne  
 48 APPLICANT: Nicholas, Scott E.  
 49 TITLE OF INVENTION: Alteration of Hemiparesis  
 50 TITLE OF INVENTION: Concentration in Plants  
 51 FILE REFERENCE: 6782  
 52 CURRENT APPLICATION NUMBER: US/09/000,803B  
 53 FILING DATE: 1999-06-22  
 54 EARLIER APPLICATION NUMBER: 60/090,416  
 55 EARLIER FILING DATE: 1998-06-23  
 56 NUMBER OF SEQ ID NOS: 9  
 57 SOFTWARE: FASTA/BLAST Release #1.0, Version #1.0  
 58 SEQ ID NO: 5  
 59 LENGTH: 28  
 60 TYPE: DNA  
 61 ORGANISM: Zea mays  
 62 US 09-890-363-4  
 63  
 64 Query Match: 45.8% Score 12.41 DB 4 Length 28:  
 65 Best Local Similarity 82.0% Prod. No. 32e+03  
 66 Matches 16, Conservation 0, Mismatches 6, Indels 0, Gaps 0

1 1 TOTGAGCAATACCTAAC 22  
 2 1 TOTGAGCAATACCTAAC 22  
 3 1 TOTGAGCAATACCTAAC 22  
 4 1 TOTGAGCAATACCTAAC 22  
 5 1 TOTGAGCAATACCTAAC 22  
 6 1 TOTGAGCAATACCTAAC 22  
 7 1 TOTGAGCAATACCTAAC 22  
 8 1 TOTGAGCAATACCTAAC 22  
 9 1 TOTGAGCAATACCTAAC 22  
 10 1 TOTGAGCAATACCTAAC 22  
 11 1 TOTGAGCAATACCTAAC 22  
 12 1 TOTGAGCAATACCTAAC 22  
 13 1 TOTGAGCAATACCTAAC 22  
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 15 1 TOTGAGCAATACCTAAC 22  
 16 1 TOTGAGCAATACCTAAC 22  
 17 1 TOTGAGCAATACCTAAC 22  
 18 1 TOTGAGCAATACCTAAC 22  
 19 1 TOTGAGCAATACCTAAC 22  
 20 1 TOTGAGCAATACCTAAC 22  
 21 1 TOTGAGCAATACCTAAC 22  
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 25 1 TOTGAGCAATACCTAAC 22  
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 30 1 TOTGAGCAATACCTAAC 22  
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 33 1 TOTGAGCAATACCTAAC 22  
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 49 1 TOTGAGCAATACCTAAC 22  
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 65 1 TOTGAGCAATACCTAAC 22  
 66 1 TOTGAGCAATACCTAAC 22  
 67 1 TOTGAGCAATACCTAAC 22  
 68 1 TOTGAGCAATACCTAAC 22  
 69 1 TOTGAGCAATACCTAAC 22  
 70 1 TOTGAGCAATACCTAAC 22  
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 76 1 TOTGAGCAATACCTAAC 22  
 77 1 TOTGAGCAATACCTAAC 22  
 78 1 TOTGAGCAATACCTAAC 22  
 79 1 TOTGAGCAATACCTAAC 22  
 80 1 TOTGAGCAATACCTAAC 22  
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 85 1 TOTGAGCAATACCTAAC 22  
 86 1 TOTGAGCAATACCTAAC 22  
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 89 1 TOTGAGCAATACCTAAC 22  
 90 1 TOTGAGCAATACCTAAC 22  
 91 1 TOTGAGCAATACCTAAC 22  
 92 1 TOTGAGCAATACCTAAC 22  
 93 1 TOTGAGCAATACCTAAC 22  
 94 1 TOTGAGCAATACCTAAC 22  
 95 1 TOTGAGCAATACCTAAC 22  
 96 1 TOTGAGCAATACCTAAC 22  
 97 1 TOTGAGCAATACCTAAC 22  
 98 1 TOTGAGCAATACCTAAC 22  
 99 1 TOTGAGCAATACCTAAC 22  
 100 1 TOTGAGCAATACCTAAC 22

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-09-890-363-4

Query Match 45.9% Score 12.4; DB 3; Length 19;  
 Best local similarity 92.9% Freq. No. 2.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

3 CTGAGCAATACCTA 16  
 5 CTGAGCAATACCTA 18

RESULT 36  
 US-09-890-363-4  
 Sequence 10, Application US/09/070964  
 Patent No. 6017730  
 GENERAL INFORMATION:  
 APPLICANT: MOLIN, Soren  
 APPLICANT: GISKOV, Michael  
 APPLICANT: KRISTENSEN, Claus S  
 APPLICANT: BEJ, Asim K  
 APPLICANT: EBERL, Leo  
 TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF  
 TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Broadway and Newark  
 STREET: 419 Seventh St., N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: United States of America  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 09/070964  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/115,065  
 FILING DATE: 13 OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COOPER, Peter P  
 REGISTRATION NUMBER: 28,005  
 REFERENCE/DOCKET NUMBER: MOLIN-6A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202 629 5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (synthetic)  
 US-09-890-363-4

Query Match 45.9% Score 12.4; DB 3; Length 19;  
 Best local similarity 92.9% Freq. No. 2.8e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

3 CTGAGCAATACCTA 16  
 15 CTGAGCAATACCTA 2

RESULT 37  
 US-09-890-363-4  
 Sequence 11, Application US/09/070964  
 Patent No. 6017730  
 GENERAL INFORMATION:  
 APPLICANT: MOLIN, Soren  
 APPLICANT: GISKOV, Michael  
 APPLICANT: KRISTENSEN, Claus S  
 APPLICANT: BEJ, Asim K  
 APPLICANT: EBERL, Leo  
 TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF  
 TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Broadway and Newark  
 STREET: 419 Seventh St., N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: United States of America  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 09/070964  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/115,065  
 FILING DATE: 13 OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COOPER, Peter P  
 REGISTRATION NUMBER: 28,005  
 REFERENCE/DOCKET NUMBER: MOLIN-6A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202 629 5197  
 TELEFAX: 202 737 3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-09-890-363-4

Query Match 45.9% Score 12.4; DB 3; Length 19;  
 Best local similarity 92.9% Freq. No. 2.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

3 CTGAGCAATACCTA 16  
 5 CTGAGCAATACCTA 18

RESULT 38  
 US-09-890-363-4  
 Sequence 12, Application US/09/070964  
 Patent No. 6017730  
 GENERAL INFORMATION:  
 APPLICANT: MOLIN, Soren  
 APPLICANT: GISKOV, Michael  
 APPLICANT: KRISTENSEN, Claus S  
 APPLICANT: BEJ, Asim K  
 APPLICANT: EBERL, Leo  
 TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF  
 TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Broadway and Newark  
 STREET: 419 Seventh St., N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: United States of America  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 09/070964  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/115,065  
 FILING DATE: 13 OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COOPER, Peter P  
 REGISTRATION NUMBER: 28,005  
 REFERENCE/DOCKET NUMBER: MOLIN-6A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202 629 5197  
 TELEFAX: 202 737 3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-09-890-363-4

Query Match 45.9% Score 12.4; DB 3; Length 19;  
 Best local similarity 92.9% Freq. No. 2.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/448,604

APPLICATION NUMBER: US/09/448,604

FILING DATE: 27 NO. 6312003 1993

CLASSIFICATION: unknown

PRIOR APPLICATION DATA: 24 JUN 1994

APPLICATION NUMBER: 08/757,102

FILING DATE: unknown

APPLICATION NUMBER: EP 9597094.0

FILING DATE: 07-APR-1995

APPLICATION NUMBER: EP 944870105.5

FILING DATE: 24 JUN 1994

ATTORNEY/AGENT INFORMATION:

NAME: CASOFF, B.C.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 149 / 14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4091

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYDROTHERMAL: NO

ANTI SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 13.

US-09-448-804 53

Query Match 46.73; Score 12.6; DR 4; Length 30;

Best Local Similarity 66.73; Freq NO: 2 44.03;

Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

CY 1 TCTGACATACCTACTAGCAACATAA 27

DB 1 TAGCAATCAAAATCAATATATATATAT 27

RESULT 34

US-08-544-822-10/0

Sequence 11, Application US/08544822

Patent No. 5834233

GENERAL INFORMATION:

APPLICANT: MOLIN, Soren

APPLICANT: GISKOV, Michael

APPLICANT: KRISTENSEN, Claus S

APPLICANT: BEJ, Asim K

APPLICANT: EBERL, Leo

TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF

TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Broadway and Belmont

STREET: 419 Seventh St., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/544,822

FILING DATE: 18 October 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/135,665

FILING DATE: 13 October 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/963,251

FILING DATE: 06 April 1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P

REGISTRATION NUMBER: 29,005

REFERENCE/DOCKET NUMBER: MOLIN=6R

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-679-7197

TELEFAX: 202-737-1928

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

US-08-544-822-10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/544,822

FILING DATE: 18 October 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/135,665

FILING DATE: 13 October 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/963,251

FILING DATE: 06 April 1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P

REGISTRATION NUMBER: 29,005

REFERENCE/DOCKET NUMBER: MOLIN=6R

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-679-7197

TELEFAX: 202-737-1928

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

US-08-544-822-10

Query Match 45.93; Score 12.4; DR 2; Length 19;

Best Local Similarity 92.03; Freq NO: 2 96.03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 3 CTGACATACCTACTA 16

DB 15 CTGACATACCTACTA 2

RESULT 35

US-08-544-822-11

Sequence 11, Application US/08544822

Patent No. 5834233

GENERAL INFORMATION:

APPLICANT: MOLIN, Soren

APPLICANT: GISKOV, Michael

APPLICANT: KRISTENSEN, Claus S

APPLICANT: BEJ, Asim K

APPLICANT: EBERL, Leo

TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF

TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Broadway and Belmont

STREET: 419 Seventh St., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/544,822

FILING DATE: 18 October 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/135,665

FILING DATE: 13 October 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/963,251

FILING DATE: 06 April 1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P

REGISTRATION NUMBER: 29,005

REFERENCE/DOCKET NUMBER: MOLIN=6R

TITLE OF INVENTION: AGE DIFFERENTIATION OF FORENSIC DNA USING A  
 HYBRIDIZATION ASSAY  
 NUMBER OF SEQUENCES: 216  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHIVE P.C.  
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: 1.02/MS-DOS  
 SOFTWARE: Easelin Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/89/065,232  
 FILING DATE: 23-DEC-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: W3 PCT/EP/95/02152  
 FILING DATE: 23 JUN 1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 958/0032.0  
 FILING DATE: 07-APR-1995  
 APPLICATION NUMBER: EP 948/0106.5  
 FILING DATE: 24 JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SALOFF, B.J.  
 REGISTRATION NUMBER: 36,663  
 REFERENCE/SECRET NUMBER: 1487-14  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-847 4701  
 TELEFAX: 703-816-4100  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 50 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 Molecule type: cDNA  
 HYDROTHERMAL: NO  
 ANTI GENSE: NO  
 US-09-765-332-53  
 Query Match: 34.0%, score 1000, 18 3, length 107  
 Best Local Similarity: 66.7%, Freq. No. 2,4003;  
 Matches: 18; Conservative: 0; Mismatches: 9; Indels: 0; Ups: 1  
 0Y 1 TCTGAGCAATACCTCAAGCAACAAAT 27  
 LB 1 TACAAAGGAAAGGAGGAGGAGGAGG 27  
 RESULT 33  
 US-09 449 894 53  
 Sequence 52, Application: 1007448334  
 Patent No: 6312903  
 GENERAL INFORMATION:  
 APPLICANT: JAMES, GERT  
 POSAV, RUDI  
 VAN HEYEROWY, HUGO  
 TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION  
 AND DIFFERENTIATION OF ENVIRONMENTAL DNA USING A  
 HYBRIDIZATION ASSAY  
 NUMBER OF SEQUENCES: 116  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHIVE P.C.  
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA

RESULT 28  
US-09-446-047A 9/c  
Sequence 9, Application US/09446047A  
Patent No. 6179924

## GENERAL INFORMATION:

APPLICANT: Darrill Sleep  
Delta Biotechnology Limited  
TITLE OF INVENTION: Improved Protein Expression Strains  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Aventis Behring LLC  
STREET: 1020 First Avenue  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: United States of America  
ZIP: 19406-1316  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/446,047A  
FILING DATE: 15-Dec-1999  
INFORMATION FOR SEQ. IT NO. 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE: TTTTAACTAAGCAATAATA 24

US-09 446 047A-9  
Query Match  
Best local similarity: 47.4%; Score 12.6; DB 4; Length 33;  
Mismatch 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  
1 TTTTAACTAAGCAATAATA 24  
DB 29 TTTTAACTAAGCAATAATA 6

RESULT 29  
US-09-311-311C-4  
Sequence 4, Application US/0931111C  
Patent No. 618738

## GENERAL INFORMATION:

APPLICANT: Erikson, et al  
TITLE OF INVENTION: POLY-BX THERAPEUTIC COMPOSITIONS,  
TITLE OF INVENTION: METHODS, AND USES THEREFOR  
FILE REFERENCE: 1874/117  
CURRENT APPLICATION NUMBER: US/09/311,311C  
CURRENT FILING DATE: 1999-05-13  
PRIOR APPLICATION NUMBER: US 61/065,106  
PRIOR FILING DATE: 1998-05-13  
NUMBER OF SEQ. IT NO.: 27  
SOFTWARE: PatentIn Release #1.0  
COUNTRY: USA  
LENGTH: 26  
TYPE: DNA  
ORGANISM: PCR primer  
FEATURE:  
US-09-311-311C 4

Query Match  
Best local similarity: 46.7%; Score 12.6; DB 4; Length 26;  
Mismatch 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY  
9 AATACTAAGCAATAATA 27  
DB 6 AATACTAAGCAATAATA 24

RESULT 30  
US-08-664-040-4694  
Sequence 4694, Application US/08664040  
Patent No. 6346398

## GENERAL INFORMATION:

APPLICANT: Favco, Pamela  
APPLICANT: Mesjigen, James  
APPLICANT: Slinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OF  
TITLE OF INVENTION: GENITING RELATED TO LEVENS  
TITLE OF INVENTION: OF VAGINAR ENDOPHYLIA:  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: Storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM EBC 260 2.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/664,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 18/000,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. IT NO.: 4694:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The letter "N" represents the base N region  
US-08-664-040-4694

Query Match  
Best local similarity: 46.7%; Score 12.6; DB 4; Length 27;  
Mismatch 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY  
6 AGCAATAGCAATAATA 25  
DB 1 AGCAATAGCAATAATA 20

RESULT 31  
US-09-045-1002  
Sequence 1002, Application US/090451002  
Patent No. 6160934

ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 STREET: 7733 FORESYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MO  
 COUNTRY: USA  
 ZIP: 63105

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/118,608

FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 971486  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 314 727 5188  
 TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 145:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 US-09-931 859E 145

Query Match 47.4% Score 12.87 DB 4 Length 25  
 Best Local Similarity 97.5% Pred. No. 1.9e+03  
 Matches 14, Conservative 9, Mismatches 2, Indels 0, Gaps 0

3 CTAGGCAATACCTAAC 18  
 21 CTAGGCAATACCTAAC 6

RESULT 26  
 US-09-931-739-145/C  
 Sequence 145, Application US/09/118,608  
 Patent No. 6232449  
 GENERAL INFORMATION:  
 APPLICANT: JOHNSON OF, EUGENE M.  
 MILBRANDT, JEFFREY D.  
 KOTZBAUER, PAUL T.  
 LAMPE, PATRICIA A.  
 TITLE OF INVENTION: HEMICELLULOSE AND RELATED COMPOUNDS WITH HATLICH  
 NUMBER OF SEQUENCES: 1/6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 STREET: 7733 FORESYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: USA  
 ZIP: 63105-1817

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/118,608  
 FILING DATE: 31-Aug-1998  
 CLASSIFICATION: Unknown

PRIMER APPLICATION DATA:  
 APPLICATION NUMBER: 9711933  
 FILING DATE: Unknown  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 971486  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 145:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 SEQUENCE INFORMATION: SEQ ID NO: 145:  
 US-09-931-739-145

Query Match 47.4% Score 12.87 DB 4 Length 25  
 Best Local Similarity 97.5% Pred. No. 1.9e+03  
 Matches 14, Conservative 9, Mismatches 2, Indels 0, Gaps 0

3 CTAGGCAATACCTAAC 18  
 21 CTAGGCAATACCTAAC 6

RESULT 27  
 US-09-128 026 145/C  
 Sequence 145, Application US/09/128,026  
 Patent No. 6403315  
 GENERAL INFORMATION:  
 APPLICANT: JOHNSON OF, EUGENE M.  
 MILBRANDT, JEFFREY D.  
 KOTZBAUER, PAUL T.  
 APPLICANT: LAMPE, PATRICIA A.  
 TITLE OF INVENTION: HEMICELLULOSE AND RELATED COMPOUNDS WITH HATLICH  
 NUMBER OF SEQUENCES: 1/6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 STREET: 7733 FORESYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: USA  
 ZIP: 63105-1817

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/128,026  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 971486  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 145:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 US-09-128 026-145

Query Match 47.4% Score 12.87 DB 4 Length 25  
 Best Local Similarity 97.5% Pred. No. 1.9e+03  
 Matches 14, Conservative 9, Mismatches 2, Indels 0, Gaps 0

3 CTAGGCAATACCTAAC 18  
 21 CTAGGCAATACCTAAC 6



APPLICATION NUMBER: US/08/482,182  
 FILING DATE: 07 JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARK, FREDDIE K.  
 REGISTRATION NUMBER: 35,636  
 REFERENCE/DOC# NUMBER: 2004, 2006, 2007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 811-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 20:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-482-182-20

Query Match 47.4% Score 12.9 DP 2 Length 20  
 Best Local Similarity 87.5% Find No. 1,84,031  
 Matches 14 Conservative 0 Mismatches 2 Indels 0 Gaps 0

QY 3 CTGACCATACCTAAC 18  
 17 CTGACCATACCTAAC 2

RESULT 21  
 US-08-482-182-21  
 Sequence 63, Application US/08482182  
 Patent No. 5861273  
 GENERAL INFORMATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OLSON, PAMELA S.  
 TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS  
 TITLE OF INVENTION: GENES IN BACTERIAL CELLS  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FORESTER  
 STREET: 765 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304 1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/482,182  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARK, FREDDIE K.  
 REGISTRATION NUMBER: 35,636  
 REFERENCE/DOC# NUMBER: 2004, 2006, 2007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 811-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 63:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-482-182-63

Query Match 47.4% Score 12.9 DP 2 Length 20  
 Best Local Similarity 87.5% Find No. 1,84,031  
 Matches 14 Conservative 0 Mismatches 2 Indels 0 Gaps 0

QY 3 CTGACCATACCTAAC 18  
 17 CTGACCATACCTAAC 2

RESULT 24  
 US-08-445-2928-23  
 Sequence 23, Application US/08445289R  
 Patent No. 5693467  
 GENERAL INFORMATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FOLLIOT, RICHARD O.  
 TITLE OF INVENTION: A Yeast Strain For Efficient Growth Under A  
 TITLE OF INVENTION: Set of Mixed and Single Sequence Primers  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: American Type Culture Collection  
 STREET: 12301 Parkway Drive  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: U.S.A.  
 ZIP: 20852  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/445,289R  
 FILING DATE: 19-MAY-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BADE, ANNETTE L.  
 REGISTRATION NUMBER: 37,609  
 REFERENCE/DOC# NUMBER: P000003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-231-6520  
 TELEFAX: 301-816-4366  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 21 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-445-289R-23

Query Match 47.4% Score 12.9 DP 1 Length 21  
 Best Local Similarity 87.5% Find No. 1,84,031  
 Matches 14 Conservative 0 Mismatches 2 Indels 0 Gaps 0

QY 4 TGAACATACCTAAC 19  
 5 TGAACATACCTAAC 20

RESULT 25  
 US-08-931-8598-145/C  
 Sequence 145, Application US/08931859E  
 Patent No. 6,223,322  
 GENERAL INFORMATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JOHNSON, EUGENE M.  
 TITLE OF INVENTION: A Yeast Strain For Efficient Growth Under A  
 TITLE OF INVENTION: Set of Mixed and Single Sequence Primers  
 NUMBER OF SEQUENCES: 239  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: American Type Culture Collection  
 STREET: 12301 Parkway Drive  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: U.S.A.  
 ZIP: 20852  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/931,859E  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JOHNSON, EUGENE M.  
 REGISTRATION NUMBER: 37,609  
 REFERENCE/DOC# NUMBER: P000003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-231-6520  
 TELEFAX: 301-816-4366  
 INFORMATION FOR SEQ ID NO: 145:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 21 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-931-8598-145/C

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? INFORMATION FOR SEQ ID NO: 18
? SEQUENCE CHARACTERISTICS:
? LENGTH: 19 bases
? TYPE: Nucleic acid
? STRANDEDNESS: Single
? TOPOLOGY: Linear
? MOLECULE TYPE: Other nucleic acid
? DESCRIPTION: 17 terminal cytosine
? HYPOTHEetical: NO
? ANTI-SENSE: Yes
? PCT:US96-05611A 18

Query Match 47.41, Score 12.67, DB 57, Length 19
Best Local Similarity 97.87, Field No. 1,981,037
Matches 14, Conservation 0, Mismatches 0, Indels 0, Gaps 0

CY 3 CTGAGCAATACCTAAC 18
DB 16 CTGAGCAATACCTAGC 1

RESULT 20
US-08-170-688-6/c
? Sequence 6, Application US/08170688
? Patent No. 5470727
? GENERAL INFORMATION:
? APPLICANT: MACCARENHAS, DESMOND
? APPLICANT: OLSON, PAMELA S.
? TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
? TITLE OF INVENTION: GENES IN BACTERIAL CELLS
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FORSTER
? STREET: 755 Page Mill Road
? CITY: Palo Alto
? STATE: California
? COUNTRY: USA
? ZIP: 94304-1018
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 21 DEC 1993
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: PARK, FREDDIE K.
? REGISTRATION NUMBER: 35,636
? REFERENCE/DOC#ET NUMBER: 22095-00291.00
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 913-5600
? TELEFAX: (415) 494-0792
? TELEX: 706141
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 20 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-170-588-6

Query Match 47.41, Score 12.67, DB 57, Length 20
Best Local Similarity 97.87, Field No. 1,981,037
Matches 14, Conservation 0, Mismatches 0, Indels 0, Gaps 0

CY 3 CTGAGCAATACCTAAC 18
DB 17 CTGAGCAATACCTAGC 2

RESULT 21

```

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US-08-182-182-6/c
? Sequence 6, Application US/08182182
? Patent No. 5861273
? GENERAL INFORMATION:
? APPLICANT: MACCARENHAS, DESMOND
? APPLICANT: OLSON, PAMELA S.
? TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
? TITLE OF INVENTION: GENES IN BACTERIAL CELLS
? NUMBER OF SEQUENCES: 81
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FORSTER
? STREET: 755 Page Mill Road
? CITY: Palo Alto
? STATE: California
? COUNTRY: USA
? ZIP: 94304-1018
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: PARK, FREDDIE K.
? REGISTRATION NUMBER: 35,636
? REFERENCE/DOC#ET NUMBER: 22095-00291.00
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 913-5600
? TELEFAX: (415) 494-0792
? TELEX: 706141
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 20 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-182-182-6

Query Match 47.41, Score 12.67, DB 57, Length 20
Best Local Similarity 97.87, Field No. 1,981,037
Matches 14, Conservation 0, Mismatches 0, Indels 0, Gaps 0

CY 3 CTGAGCAATACCTAAC 18
DB 17 CTGAGCAATACCTAGC 2

RESULT 22
US-08-182-182-20/c
? Sequence 6, Application US/08182182
? Patent No. 5861273
? GENERAL INFORMATION:
? APPLICANT: MACCARENHAS, DESMOND
? APPLICANT: OLSON, PAMELA S.
? TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
? TITLE OF INVENTION: GENES IN BACTERIAL CELLS
? NUMBER OF SEQUENCES: 81
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FORSTER
? STREET: 755 Page Mill Road
? CITY: Palo Alto
? STATE: California
? COUNTRY: USA
? ZIP: 94304-1018
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:

```

TOPOLOGY: linear  
ID: 257-772-41

Query Match: 48.1% Score 13, DB 4; Length 15,  
Best Local Similarity: 76.2%, Pred. No. 1.6e+03,  
Matches: 14, Conservative: 9, Mismatches: 1, Indels: 0,

Tags: 0,

QY 4 CTGAGTAACTAACTAAC 24  
ID 10 CTGAGTAACTAACTAAC 10

RESULT 17

US-09-070-408-131/c  
Sequence: 131, Application US/09/070408  
Patent No. 6180441

GENERAL INFORMATION:

APPLICANT: Iversen, Brent L.

APPLICANT: Ralston, George

TITLE OF INVENTION: IN VITRO CLONING SATURATION MUTAGENESIS

TITLE OF INVENTION: OF PROTEINS

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSER: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,408

FILING DATE: Concurrently Herewith

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: US 69/946,409

FILING DATE: 01 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: McMillan, Napoleon F.

PRECEDENCE NUMBER: P-43,363

REFERENCE/SECRET NUMBER: US/09-070

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418 3000

TELEFAX: 512/447 7577

INFORMATION FOR SEQ ID NO: 131

SEQUENCE CHARACTERISTICS:

LENGTH: 13 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-070-408-131

Query Match: 47.4% Score 12.8, DB 4; Length 15,  
Best Local Similarity: 87.5%, Pred. No. 1.6e+03,  
Matches: 14, Conservative: 9, Mismatches: 2, Indels: 0,  
Tags: 0,

QY 3 CTGAGTAACTAACTAAC 18  
ID 16 CTGAGTAACTAACTAAC 1

RESULT 18

US-09-131-028A-16/c

Sequence: 16, Application US/09131028A

Patent No. 679286/6

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mukerji, Pradip

APPLICANT: Lemmel, Steven A.

APPLICANT: Leonard, Amanda Eun Young

APPLICANT: Chaudhary, Sunita

TITLE OF INVENTION: 3D/4 SCHEM EXHIBITION SYSTEMS

FILE REFERENCE: 6004 US, P1

CURRENT APPLICATION NUMBER: US/09/070,408A

CURRENT FILING DATE: 1998-08-07

PRIOR APPLICATION NUMBER: US 68/064,440

PRIOR FILING DATE: 1993-05-21

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 16

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer F074

US-09-131-028A-16

Query Match: 47.4% Score 12.8, DB 4; Length 15,  
Best Local Similarity: 87.5%, Pred. No. 1.6e+03,  
Matches: 14, Conservative: 9, Mismatches: 2, Indels: 0, Tags: 0,

QY 3 CTGAGTAACTAACTAAC 18  
ID 16 CTGAGTAACTAACTAAC 1

RESULT 19

PCT-US96-05611A-18/c

Sequence: 18, Application PCT/US9605611A

GENERAL INFORMATION:

APPLICANT: Mueller, John P.

APPLICANT: Leonard, Michael J.

APPLICANT: McFarland, Henry F.

APPLICANT: Matys, Louis A.

APPLICANT: Mueller, Elven Elliott

APPLICANT: Nye, Steven H.

APPLICANT: Pellety, Clara M.

APPLICANT: Squinto, Stephen P.

APPLICANT: Wilkins, James A.

TITLE OF INVENTION: Modified Myelin Protein Moieties

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSER: Maurice M. Klee

STREET: 1901 Burr Street

CITY: Fairfield

STATE: Connecticut

COUNTRY: USA

ZIP: 06430

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 0.8 Mb Storage

COMPUTER: Macintosh Centris 510

OPERATING SYSTEM: System 7

SOFTWARE: Macintosh Word 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/05611A

FILING DATE: 02 MAY 1995

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: 08/431,644

FILING DATE: May 2, 1995

APPLICATION NUMBER: 08/431,648

FILING DATE: May 2, 1995

APPLICATION NUMBER: 08/482,114

FILING DATE: June 7, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Klee, Maurice M.

REGISTRATION NUMBER: 30,199

REFERENCE/SECRET NUMBER: ALX 123

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 254-1400

TELEFAX: (203) 254-1101



Matches 18, Conservative 0, Mismatches 8, Indels 0, Gaps 0

QY 2 CCGAGCAATACCTAACCAATA 27

10 2 CCGAGCAATACCTAACCAATA 27

RESULT 11

US-08-896-176 7

Sequence 9, Application US/0804176

Patent No. 5985581

GENERAL INFORMATION:

APPLICANT: Nixon, Ralph A.

APPLICANT: Cataldo, Anne M.

APPLICANT: Rao, Benjamin B.

APPLICANT: Mathews, Paul M.

TITLE OF INVENTION: USE OF PRESENTIN 1 FOR DIAGNOSIS OF

FILE REFERENCE: 04841/028002

CURRENT FILING DATE: 1997-07-17

EARLIER APPLICATION NUMBER: 60/022,594

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 7

LENGTH: 28

TYPE: DNA

ORGANISM: Homo sapiens

US-08-896-176 7

Query Match 48.94, Score 13.2, DP 3, Length 29;

Best Local Similarity 81.31, Field No. 1,126+03,

Matches 19, Conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 2 CCGAGCAATACCTAACCAATA 19

10 11 CCGAGCAATACCTAACCAATA 28

RESULT 12

US-09-251-565 11

Sequence 11, Application US/09251565

Patent No. 6110073

GENERAL INFORMATION:

APPLICANT: Payco, Patricia F. et al., Applied Pl. Systems Division

TITLE OF INVENTION: Complied Application and Ligation Method

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESS: David J. Woltz, Wilson-Schmidt Goodrich & Fosatti

STEPPER, 670 Elm Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1050

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: Microsoft Windows 98/MS-DOS 5.0

SOFTWARE: WordPerfect for Windows 6.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/075,932

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/075,932

FILING DATE: 19 AUG 94

ATTORNEY/AGENT INFORMATION:

NAME: David J. Woltz

REGISTRATION NUMBER: 18,162

REFERENCE/DOCKET NUMBER: 16842-754

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 493-9100

TELEFAX: (650) 493-6811

INFORMATION FOR SEQ. ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 nucleotides

TYPE: nucleic acid

STANDARDIZATION: single

TOPOLOGY: linear

US-09-251-565-11

Query Match 48.94, Score 13.2, DP 3, Length 18;

Best Local Similarity 69.23, Field No. 1,26+03,

Matches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 2 CCGAGCAATACCTAACCAATA 27

10 2 CCGAGCAATACCTAACCAATA 27

RESULT 13

US-09-081-576-9

Sequence 9, Application US/09081576A

Patent No. 6180111

GENERAL INFORMATION:

APPLICANT: Stein, Daniel C.

TITLE OF INVENTION: VACCINE DELIVERY SYSTEM

FILE REFERENCE: 2747 0097 27 CIP (8014-014)

CURRENT APPLICATION NUMBER: US/09/081,576A

CURRENT FILING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: US 08/236,422

PRIOR FILING DATE: 1997-03-23

PRIOR APPLICATION NUMBER: US 08/443,514

PRIOR FILING DATE: 1995-05-18

NUMBER OF SEQ. ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ. ID NO 9

LENGTH: 35

TYPE: DNA

ORGANISM: Neisseria gonorrhoeae

US-09-081-576-9

Query Match 48.94, Score 13.2, DP 4, Length 19;

Best Local Similarity 81.31, Field No. 1,126+03,

Matches 19, Conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 2 CCGAGCAATACCTAACCAATA 26

10 12 CCGAGCAATACCTAACCAATA 29

RESULT 14

US-08-544-040-6756

Sequence 6756, Application US/08544040

Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Payco, Pamela

APPLICANT: Mawzygen, James

APPLICANT: Stinchcomb, Dan T.

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES OR

TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: OF VASOTILIN PROTEIN

NUMBER OF SEQUENCES: 6002

CORRESPONDENCE ADDRESS:

ADDRESS: Lynn S. Lynn

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.50 INCH DISKETTE  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MICROSOFT WINDOWS 95  
 SOFTWARE: MICROSOFT WORD 7.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 09/06/700,403  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/745,008  
 FILING DATE: NOVEMBER 8, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FLOYD, LINDA AARNEIN  
 REGISTRATION NUMBER: 33,692  
 REFERENCE/DOCKET NUMBER: NO. 1007 A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 302-692-8112  
 TELEFAX: 302-773-0164  
 INFORMATION FOR SEQ ID NO: 64:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 26 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-766-439-68

Query Match: 48.9% Score 13.2; DB 2; Length 26  
 Identical Similarity: 93.8%; Ident. No. 1.2e+03;  
 Matches: 19; Conservative: 0; Mismatches: 1; Indels: 0; Type: 0

CY 9 AATACCTAGACGACAAAT 26  
 DB 2 AATCCTAGACGACAAAT 13

RESULT 9  
 US-08-584-040-3413  
 Sequence 3413, Application US/08594040  
 Patent No. 6346398  
 GENERAL INFORMATION:  
 APPLICANT: PAVON, Pamela  
 APPLICANT: KOSWIG, James  
 APPLICANT: Stinchcomb, Dan T  
 APPLICANT: Eschbold, Jaime  
 TITLE OF INVENTION: METHOD AND APPARATUS FOR THE  
 TREATMENT OF DISEASES OF  
 TITLE OF INVENTION: CONJUGATE FRAGMENTED LIBROS  
 TITLE OF INVENTION: SEWAGE TREATMENT  
 TITLE OF INVENTION: SEWAGE TREATMENT  
 NUMBER OF SEQUENCES: 8502  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: 1500 S. 1500  
 STREET: 603 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 TELEPHONE: 213-621-1066  
 TELEFAX: 213-621-1066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 MEDIUM TYPE: Storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM PC DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 09/09/584,040  
 FILING DATE: January 11, 1998  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 68/005,974  
 FILING DATE: October 26, 1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard D  
 REGISTRATION NUMBER: 42,007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 452-1500  
 TELEFAX: 212 452-1500  
 TELEX: 67-3610  
 INFORMATION FOR SEQ ID NO: 3413:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 OTHER INFORMATION: The letter "N" represents the adenine region  
 of the 19-24 region of the 1.1 kbp 1.1 kbp.  
 US-08-591-040-2413

Query Match: 48.9% Score 13.2; DB 4; Length 27  
 Identical Similarity: 63.0%; Ident. No. 1.2e+03;  
 Matches: 12; Conservative: 3; Mismatches: 4; Indels: 1; Type: 0

CY 8 CAATACGACGACAAAT 26  
 DB 3 CAATACGACGACAAAT 21

RESULT 10  
 US-08-591-040-2413  
 Sequence 2413, Application US/08597902  
 Patent No. 5912148  
 GENERAL INFORMATION:  
 APPLICANT: Perkin Elmer Corporation, Applied Biosystems Division  
 TITLE OF INVENTION: Coupled amplification and ligation method  
 NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David J. Woltz, Wilson Scientific Goodrich & Renard  
 STREET: 650 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1050  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: Microsoft Windows 95  
 SOFTWARE: WordPerfect for Windows 6.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08-591-040-2413  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/292,696  
 FILING DATE: 19-AUG-94  
 ATTORNEY/AGENT INFORMATION:  
 NAME: David J. Woltz  
 REGISTRATION NUMBER: 38,362  
 REFERENCE/DOCKET NUMBER: PELM4215  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 493-9300  
 TELEFAX: (415) 493-6811  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-975-902-11

Query Match: 48.9% Score 13.2; DB 2; Length 28  
 Identical Similarity: 67.2%; Ident. No. 1.2e+03;

## SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-08-439-628-02

Query Match 16.44, Score 13.6, ID 2, Length 31,  
 Best Local Similarity 90.0%, Freq. No. 8,40+35,  
 Matches 16, Conservative 0, Mismatches 4, Indels 0,

QY 2 CTATACATACCATACAA 21  
 DB 22 CTATACATACCATACAA 3

## RESULT 6

US-07-662-764D-14

Sequence 14, Application us/076627641

Patent No. 5664141

GENERAL INFORMATION:

APPLICANT: FISHBARK, GEORGE

TITLE OF INVENTION: METHOD AND MEANS FOR SETTING AND

TITLE OF INVENTION: IDENTIFYING MOLECULAR INFORMATION

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: LERER, DAVID, LITTEBERG, RONALD &

ADDRESSEE: MENTHIR

STREET: 600 South, Avenue West

CITY: Westfield

STATE: New Jersey

COUNTRY: USA

ZIP: 07090

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: P4-01 in Release #1.0, Version #1.10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/662,764D

FILING DATE: 28 FEB 1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/201,358

FILING DATE: 26 MAY-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/770,300

FILING DATE: 28 AUG 1985

ATTORNEY/AGENT INFORMATION:

NAME: Foley, Shawn P.

REGISTRATION NUMBER: 33,071

REFERENCE/DOCKET NUMBER: LITTEB/0002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5000

TELEFAX: 908-654-7866

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-662,764D-14

Query Match 48.98, Score 13.7, ID 2, Length 21,  
 Best Local Similarity 93.3%, Freq. No. 1,00+33,  
 Matches 15, Conservative 0, Mismatches 3, Indels 0,

QY 8 CTAATCTAACCAACAA 25  
 DB 4 CTAATCTAACCAACAA 21

## RESULT 7

US-08-766-439-67

Sequence 67, Application us/08766439

Patent No. 592538

GENERAL INFORMATION:

APPLICANT: HAZEL, JAMES WILLIAM

APPLICANT: JENSEN, MARK ANTON

TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR

TITLE OF INVENTION: THE DETECTION OF LISTERIA

TITLE OF INVENTION: WISCONSIN AND LISTERIA SPT.

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.50 INCH DISKETTE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WINDOWS 3.1

SOFTWARE: MICROSOFT WORD 6.00

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/766,439

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/745,228

FILING DATE: NOVEMBER 8, 1996

ATTORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AXAMETHY

REGISTRATION NUMBER: 23,692

REFERENCE/DOCKET NUMBER: MD-1065-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-9112

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-766-439-67

Query Match 49.98, Score 13.7, ID 2, Length 26,  
 Best Local Similarity 83.3%, Freq. No. 1,20+03,  
 Matches 15, Conservative 0, Mismatches 3, Indels 0,

QY 9 AATACCTAACCAACAAI 26  
 DB 2 AATACCTAACCAACAAI 19

RESULT 8

US-08-766-439-68

Sequence 68, Application us/08766439

Patent No. 592538

GENERAL INFORMATION:

APPLICANT: HAZEL, JAMES WILLIAM

APPLICANT: JENSEN, MARK ANTON

TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR

TITLE OF INVENTION: THE DETECTION OF LISTERIA

TITLE OF INVENTION: WISCONSIN AND LISTERIA SPT.

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: U.S.A.

ZIP: 19898









685	10.4	31.4	15.4	US-08-646-855-11	Sequence 11, Aff1	754	10	37.0	23	1	US-08-656-716-40	Sequence 41, Aff1
686	10.2	31.8	35.4	US-08-590-061-17	Sequence 17, Aff1	755	10	37.0	23	2	US-08-637-715-33	Sequence 41, Aff1
688	10.2	31.8	35.4	US-08-731-466-10	Sequence 10, Aff1	756	10	37.0	23	3	US-08-446-924-16	Sequence 16, Aff1
689	10	31.0	14.4	US-08-646-449-64	Sequence 64, Aff1	757	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
690	10	31.0	14.4	US-08-754-147-132	Sequence 132, Aff1	758	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
691	10	31.0	14.4	US-08-754-147-132	Sequence 132, Aff1	759	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
692	10	31.0	14.4	US-08-754-147-132	Sequence 132, Aff1	760	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
693	10	31.0	14.4	US-08-446-500-17	Sequence 17, Aff1	761	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
694	10	31.0	14.4	US-08-446-500-17	Sequence 17, Aff1	762	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
695	10	31.0	14.4	US-08-446-500-17	Sequence 17, Aff1	763	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
696	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	764	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
697	10	31.0	14.4	US-08-941-155-13	Sequence 13, Aff1	765	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
698	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	766	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
699	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	767	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
700	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	768	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
701	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	769	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
702	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	770	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
703	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	771	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
704	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	772	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
705	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	773	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
706	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	774	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
707	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	775	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
708	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	776	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
709	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	777	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
710	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	778	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
711	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	779	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
712	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	780	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
713	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	781	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
714	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	782	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
715	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	783	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
716	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	784	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
717	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	785	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
718	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	786	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
719	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	787	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
720	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	788	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
721	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	789	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
722	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	790	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
723	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	791	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
724	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	792	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
725	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	793	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
726	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	794	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
727	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	795	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
728	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	796	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
729	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	797	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
730	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	798	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
731	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	799	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
732	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	800	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
733	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	801	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
734	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	802	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
735	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	803	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
736	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	804	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
737	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	805	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
738	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	806	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
739	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	807	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
740	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	808	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
741	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	809	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
742	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	810	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
743	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	811	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
744	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	812	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
745	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	813	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
746	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	814	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
747	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	815	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
748	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	816	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
749	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	817	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
750	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	818	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
751	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	819	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
752	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	820	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
753	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	821	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
754	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	822	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
755	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	823	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
756	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	824	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
757	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	825	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
758	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	826	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
759	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	827	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
760	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	828	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
761	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	829	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
762	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	830	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
763	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	831	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
764	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	832	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
765	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	833	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
766	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	834	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
767	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	835	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
768	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	836	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
769	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	837	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
770	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	838	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
771	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	839	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
772	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	840	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
773	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	841	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
774	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	842	10	37.0	23	4	US-08-446-924-16	Sequence 16, Aff1
775	10	31.0	14.4	US-08-643-212-39	Sequence 39, Aff1	843	10	37.0				





[illegible]







2. Via pro-mitogens. The TrkA? subdomain comprises a portion of the extracellular domain of TrkA. The Ig-like subdomain 2 is the portion of TrkA responsible for binding neurotrophins such as nerve growth factor (NGF). TrkA? binds NGF with high affinity, inhibiting its biological activity *in vitro* and *in vivo*. NGF is one of a family of neurotrophins involved in the development and maintenance of the peripheral and central nervous system, being a potent neurotrophic factor for certain cholinergic neurons and promoting the survival and differentiation of sympathetic and sensory neurons during development. NGF also acts as a mediator of some persistent pain states by interacting with TrkA receptors of a subpopulation of nociceptive sensory neurons of the dorsal root ganglion. The action of NGF on TrkA receptors causes an increase in neuropeptide levels in these sensory neurons and affects sodium and calcium channels such that these neurons are increased in excitability. In chronic inflammatory states (e.g., arthritis, bladder cystitis), the effects of persistently elevated NGF levels result in a long-term disabling pain state. NGF upregulation is also likely to be involved in post-herpetic neuralgia which is associated with shingles. TrkA-derived peptides which bind NGF can be used to reduce NGF levels and thus to treat pain associated with NGF (or other neurotrophin) upregulation e.g., pain symptomatic of idiopathic sensory urgency, interstitial cystitis, arthritis, shingles, peripheral inflammation, chronic inflammation or postherpetic neuralgia. They may be used to screen for molecules that bind to TrkA, to identify molecules that enhance binding to a neurotrophin, to identify neurotrophin analogues, and may be administered therapeutically to treat patients with Alzheimer's disease. TrkA peptides and nucleotides are also useful as diagnostic probes.

XX	
SQ	Sequence 19 BP; 3 A; 4 C; 6 G; 6 T; 0 other;

Query Match	47.4%	Score 12.9	SP 21	Length 19
Best Local Similarity	87.5%	Pred. No. 1.6e+04		
Matches 14	Conservative 0	Mismatches 2	Indels 0	Gaps 0

2Y	3	CTGAC:CAATACCTAAC	18
2b	16	CTGAC:CAATACCTAAC	1

Search completed: July 21, 2003, 14:06:05  
Job time : 108.101 secs

CS Synthetic.  
 XX W0200004465-A1.  
 XX  
 PD 15-JUN 2000.  
 XX  
 FE 11-DEC-1999; 99W0-040102  
 XX  
 FE 18-DEC-1998; 98US-0207389.  
 XX  
 PA 1999; CONFERENCE: ELECTROPHORETIC UNIT.  
 XX  
 PI Mismatches: 2;  
 XX  
 DR WPI: 2000-422415/26.  
 XX  
 PT Isolated nucleic acid molecule for obtaining human, recombinant, in animal  
 PT encodes Nucleoside triphosphatase for 3D structure of Aspartate  
 PT Immunoglobulin Hsp60 and Gamma2 diastase Hsp60 polypeptide  
 XX  
 PS Example 7; Page 62, 118FF, English.  
 XX  
 CC The Hsp60 heat shock protein or fragment derived from a mammalian  
 CC mammalian and the Hsp60 heat shock protein fragment derived  
 CC from a prokaryotic organism or Gamma2 diastase can be used as  
 CC immunogens to five protective immunity from these microorganisms.  
 CC Nucleic acid sequences encoding these proteins are useful for  
 CC producing recombinant proteins for immunizing an animal or as  
 CC probes and/or primers to detect the microorganisms in a host cell.  
 CC sample.  
 XX  
 SC Sequence 19 BP, 3 A; 4 C; 6 G; 6 T; 0 other;  
 Query Match 1548; Date 10-5; DB 21; Length 19;  
 Best Local Similarity 8758; Prod No. 160104;  
 Matches 14; Conservativ 0; Mismatches 2; Indels 0; Gaps 0;  
 CY 3 CTGAGCAATACCTTAC 18  
 |||||  
 DB 16 CTGAGCAATACCTAGC 1  
 RESULT 19  
 AA250913/c  
 ID AA250913 standard; DNA; 19 BP.  
 XX  
 AC AA250913;  
 XX  
 DT 31-MAY-2000 (first entry)  
 XX  
 DE PCR primer R074 to amplify human beta-casein gene.  
 XX  
 KW Plasmid PRAB-84-69; recombinant; beta-casein; human; PCR primer;  
 KW casein kinase II alpha subunit; casein kinase II beta subunit;  
 KW kanamycin resistance marker; (resistance); protein stability;  
 KW pharmaceutical; nutritional composition; vaccine formulation; etc.  
 CS Homo sapiens.  
 XX  
 PN W0200008174-A1.  
 XX  
 PD 17-FEB 2000.  
 XX  
 PF 06-AUG-1999; 99W0-US17873.  
 XX  
 PR 07-AUG 1998; 98US-0141024.  
 XX  
 PA (ABBO) ABBOTT LAB.  
 XX  
 PI Mukerji P, Lemmel SA, Leonard AE, Chaudhary S;  
 XX  
 DE WPI: 2000-207017/9

PT Recombinant construct useful for producing human milk protein, alpha  
 PT plant protein, antibody, antigen or hormone, complexed nucleotide  
 PT sequences expressing beta-casein protein  
 XX  
 XX Example 1; Page 11; 73pp; English.  
 XX  
 PS The patent discloses a method of producing human milk protein, alpha  
 CC plant protein, antibody, antigen or hormone, complexed nucleotide  
 CC transforming host cells with a vector comprising the gene  
 CC of interest linked to a promoter and nucleotide sequences encoding  
 CC subunit of a kinase, proteinase, nucleic acid, and a polypeptide, and  
 CC useful for improving the genetic stability of a plasmid containing  
 CC cell during fermentation. Proteins produced may be used in  
 CC pharmaceutical or nutritional compositions and in vaccine formulations.  
 CC The present sequence is that of PCR primer R074, used to amplify human  
 CC beta-casein gene for construction of plasmid PRAB-84-69; PRAB-84-69  
 CC contains amplified gene encoding human beta casein, human kinase II  
 CC alpha and beta subunit, kanamycin resistance marker and  
 CC immunoprecipitate.  
 XX  
 SC Sequence 19 BP, 3 A; 4 C; 6 G; 6 T; 0 other;  
 Query Match 1548; Date 10-5; DB 21; Length 19;  
 Best Local Similarity 8758; Prod No. 160104;  
 Matches 14; Conservativ 0; Mismatches 2; Indels 0; Gaps 0;  
 CY 3 CTGAGCAATACCTTAC 18  
 |||||  
 DB 16 CTGAGCAATACCTAGC 1  
 RESULT 40  
 AA250248/c  
 ID AA250248 standard; DNA; 19 BP.  
 XX  
 AC AA250248;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE T7 terminator PCR primer.  
 XX  
 KW Tyrosine kinase, TKK, immunoglobulin, Ig, adhesion binding;  
 KW neurotrophin, nerve growth factor, NGF, inhibitor, pain, sensory;  
 KW sympathetic; neuron, TRKA receptor; nonreceptor; dorsal root ganglion;  
 KW chronic inflammatory states; upregulation; treatment; arthritis;  
 KW diagnostic; sensory; sensory; immunological; cytokine; stimulus;  
 KW inflammation; postherpetic neuralgia; analgesic; Alzheimer's disease;  
 KW diagnosis; splice variant; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 OS Bacteriophage T7.  
 XX  
 PN W0200005025-A2.  
 XX  
 PD 11-OCT-1999.  
 XX  
 PF 09-APR-1999; 99W0-GB01108.  
 XX  
 PR 04-APR-1998; 98GB-0007781.  
 XX  
 PA (UYBR-) UNIV BRISTOL.  
 XX  
 PI Robertson AGS, Allen SD, Dawbarn D;  
 XX  
 DR WPI: 2000-023041/02.  
 XX  
 PT Novel plasmid vector useful for creating Alzheimer's disease antigen in  
 PT e.g. arthritis, shingles etc.  
 XX  
 XX Example 2; Page 14; 67pp; English.  
 CC PCR primers AA250248 and 250249 were used to create a cDNA encoding a portion  
 CC variant of human tyrosine kinase TRKA immunoglobulin 19-180 and 180-180

Query Match 48.1% Score 137 DB 14; Length 35;  
Best Local Similarity 76.2% Pred. No. 1,46,04;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

0Y 4 TGAACATACCTAACACAA 24  
|||||  
10 TGAACATATCTTAAGAA 10

## RESULT 36

AAV26876/C

10 AAV26876 standard; DNA; 35 BP.

XX AAV26876;

XX 01-SEP-1998 (first entry)

XX Recombinant foot virus primer RM389.

XX 10-SEP-1998; Marburg disease virus; M.V. glycoprotein; vaccination;

XX ss; PCR; primer; amplification.

XX Synthetic

XX US5759553 A.

XX 02-JUN-1998.

XX 07-JUN-1998; Gene 5475673

XX 07-MAR-1994; 94US-0207792.

XX 07-MAR-1994; 94US-0666066.

XX 11-JUN-1991; 91US-0713967.

XX 13-JAN-1992; 94US-0840077.

XX 06-MAR-1992; 94US-0847951.

XX 04-JAN-1993; 94US-0001393.

XX 12-AUG-1993; 94US-0105481.

XX 07-JUN-1998; 96US-0475683.

XX (VIBO) VIRUSENERGIC CCRP.

XX Paolletti F, Ross L, Tarraglia G, Taylor J;

XX WPI; 1998 112565/23.

XX Recombinant virus containing Marburg disease virus DNA

XX for RNA vaccination of baboons (F. David G. Recombinant

XX glycoprotein).

XX Example 1: Column 19; 32pp; English.

XX The primers AAV26876-2 were used in the production of a recombinant

XX vaccine virus containing exogenous DNA encoding Marburg disease virus

XX (MDV) gp and/or gp glycoprotein. The virus is useful for protecting

XX chickens against MDV infection by DNA vaccination, or for producing

XX recombinant MDV gp and/or gp glycoproteins.

XX Sequence 35 BP; 11 A; 7 C; 3 G; 14 T; 0 other;

XX Query Match 48.1% Score 137 DB 14; Length 35;

XX Best Local Similarity 76.2% Pred. No. 1,46,04;

XX Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX 4 TGAACATACCTAACACAA 24

XX 10 TGAACATATCTTAAGAA 10

XX RESULT 37

XX AAT42788/C

XX 10 AAT42788 standard; DNA; 19 BP.

XX

AC AAT42788;

XX 01-FEB-1997 (first entry)

XX T7 terminator primer.

XX Myelin basic protein; MBP; proteolipid protein; PLP;

XX Multiple sclerosis; autoimmune disease; diagnosis; therapy;

XX T-lymphocyte; T-cell; apoptosis; primer; PCR;

XX polymerase chain reaction; ss.

XX Synthetic

XX WO9634622-A1.

XX 07-NOV-1996.

XX 22-APR-1996; 96WO-0505611.

XX 07-JUN-1995; 95US-0482114.

XX 12-MAY-1995; 95US-0416441.

XX 02-MAY-1995; 95US-0431648.

XX (ALEX-) ALEXION PHARM INC.

XX (USSH) US DEPT HEALTH &amp; HUMAN SERVICES.

XX Leonardo M, Matis L, McFarland HF, Mueller EF, Mueller OF;

XX Nye SH, Fellrey CM, Quinto SF, Wilkins JA,

XX WPI; 1996 156565/50.

XX New human myelin basic protein and proteolipid protein variant for

XX used in the assessment, diagnosis and treatment of multiple

XX sclerosis

XX Example; Page 99; 156pp; English.

XX A PCR fragment that includes the human myelin basic protein (MBP)

XX exon 2 sequence was generated from pR122/MBP28.5 (see also

XX AAT42785-96) using the sense oligonucleotide given in AAT42787 in

XX combination with an antisense primer (AAT42786) that hybridizes to

XX the 3' termination of pR122. A second PCR fragment was generated

XX from the same template with a T7 promoter primer (AAT42789) and an

XX antisense primer (AAT42790) that hybridized to the 5' end of exon

XX 2. Fusion of the PCR products by amplification with T7 promoter

XX and terminator primers completed the construction of a PCR

XX product containing the xpr-Xycep1/Nov gene from Nov AAT41893.

XX Sequence 19 BP; 4 A; 4 C; 6 G; 6 T; 0 other;

XX Query Match 47.4% Score 12.8; DB 17; Length 19;

XX Best Local Similarity 87.5% Pred. No. 1,66,04;

XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 3 CTGACATACCTAAC 18

XX 16 CTGACATATCTTAAC 1

XX RESULT 38

XX AAA49413/C

XX 10 AAA49413 standard; DNA; 19 BP.

XX AAA49413;

XX 26-SEP-2000 (first entry)

XX T7 terminator primer used for sequencing.

XX Hsp70; Hsp60; heat shock protein; immunogen; immunity; vaccination;

XX detection; Neisseria meningitidis; Aspergillus fumigatus;

XX Candida glabrata; primer; ss.

XX



```

NM_006987.1 Homo sapiens
XX XX
XX XX MO200129251 A2.
XX XX
XX XX
XX XX 26 APR 2001.
XX XX
XX XX 18 OCT 2000; genome-wide effort.
XX XX
XX XX FR 04 OCT 1999; 95EP-0870216.
XX XX FR 03-JUN-2000; Z0006P-0870122.
XX XX FR 16 JUN 2000; Z0006Ps-0211629.
XX XX
XX XX (UVEGE ) UNIV GENT.
XX XX
XX XX Mousaen L, Gallons T.
XX XX WFLJ 2001-306341/31.
XX XX
XX XX Mutation analysis of NF1 gene by treating EBV transformed
PT lymphoblastoid cell lines formed with lymphocytes of patient with
PT protein synthesis inhibition, and obtaining peptides by translating
XX amplified RNA from cell line .
XX
XX Example 7, Page 30, SEQID# ENGLISH
XX
XX The DNA sequences between nucleophilic proteinase type-1 (NF1) chromosomal
XX fragment A method for mutation analysis of the NF1 gene involves
XX isolating peripheral blood lymphocytes (PBL) of a patient, establishing
XX Epstein Barr virus (EBV) transduced B lymphoblastoid cell line with
XX isolated PBL, or other cells containing it PBL by epithelialization (PNA
XX stimulation), leading the cell line or short-term culture with protein
XX synthesis inhibitor and immediately extracting RNA from the cultures. The
XX RNA is then amplified and rapidly fragments are cloned by in vitro
XX transcription/transcription of amplified fragments. Mutation analysis of
XX NF1 is used for detection of frame shift, missense and silent mutations
XX in various cases of the gene. This is useful in screening for NF1
XX mutations in young children who are often oligosymptomatic. Efficacy of a
XX drug or agent can be identified by a screening process in which the
XX modulation is monitored in vitro using cell systems in which the
XX defective NF1 gene is expressed. The sequences can be used to design
XX drugs which modulate NF1 activity, by using knowledge of the structure of
XX the NF1 protein and of specific defects of the various NF1 mutant
XX proteins. The method allows for reliable analysis of mutations that are
XX difficult to detect due to unstable or wrong-spliced transcripts
XX
XX Sequence ID BP: 2 A; 0 C; 9 G; 20 U; 1 Other:
XX
XX Query Match 48.9%; Score 13.2; DB 22; Length 32;
XX Best local Similarity 55.0%, Field No. 114904,
XX Matches 15; Conservative 1; Mismatches 4; Indels 6; Gaps 0
XX
XX 27 CAATACCTAGCAACAATAA 27
XX ||||| |||||||
XX 27 CAAAAATATGACAAACCAACA 8
XX
XX RESULT 12
XX AAH26287
XX ID AAH26287 of release 1, CDS, 27 PEs.
XX AX
XX AX AAH26287;
XX
XX 02-OCT-2001 (first entry)
XX
XX Igs transporting to receptor alpha chain FOR primer B).
XX
XX Peptide(s): F-SG, [Lys=Ala] 4 amino acids, alk., alkaline,
XX transgenic animal; ruminant; cattle; PCR primer; ss.
XX
XX Rattus sp.
XX

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03 Mus sp.sapiens.
04 Hmo sapiens.
XX XX M000157088-A1.
XX XX
XX XX 09-AUG-2001.
XX XX
XX XX 02 FEB 2000; 2001W0 SE00202.
XX XX
XX XX 03 FEB 2000; 2000W0 SE00110.
XX XX
XX XX (HAMM/) HAMMARSTROM L.
XX XX (KACS/) KACSKOVICS I.
XX XX
XX XX Hammarstrom L. Kacskovics I.
XX XX
XX XX WPI; 2001-493419/52.
XX XX
XX XX New DNA molecule encoding immunoglobulin G transporting human Fc
XX XX receptor, FcRn, useful for producing polypeptide of mice with enhanced
XX XX levels of immunoglobulins or proteins fused to immunoglobulin heavy
XX XX chains.
XX XX
XX XX Disclosures: Page 6, 4ff, English.
XX XX
XX XX The present sequence is that of degenerate primer B4, which is
XX XX based on a region of homology between rat, mouse and human Fc
XX XX transporting Fc receptor (FcRn) alpha-chain sequences. He was
XX XX used with primer B3 (see AM05292) in the RT-PCR amplification of
XX XX alpha-1.1999 derived cDNA. A segment spanning the alpha-1.1
XX XX alpha-2 and alpha-3 extracellular domains of FcRn was obtained.
XX XX Subsequent PCR analysis of primer B3 provided a full length
XX XX sequence (see AM05294) for alpha FcRn (see AM05294). The
XX XX invention relates to a human major histocompatibility complex
XX XX class II-like protein, an alpha-1.1-like chain, and other FcRn
XX XX RNA molecules, and the proteins encoded by them. It also provides
XX XX a method of producing mice or polypeptides with enhanced levels of
XX XX immunoglobulins or proteins fused to immunoglobulin gamma chains or
XX XX their FcRn interacting regions.
XX XX
XX XX Sequence 22 BP, 7 A, 6 C, 3 G, 3 T, 3 other;
XX XX
XX XX Query March 48 14; Score 13; DB 22; Length 203
XX XX Best local similarity for 48; Prod No. 1,39404;
XX XX Matches 22; Conservation 0; Vector-Seq 0; Indel 0; Gaps
XX XX
XX XX 6 AAAAAAAAAAAATTAATAA 24
XX XX |||||:|:|:|:|:|:|
XX XX 4 AAAAAAAAAATGASTACAA 22
XX XX
XX XX RESULT 33
XX XX AA162188/c
XX XX ID AA162188 standard; DNA: 25 BP
XX XX
XX XX AA162188:
XX XX
XX XX 16-OCT-2001 (first entry)
XX XX
XX XX Soybean 319013 region A1 ENA forward primer, SEQ ID NO: 819.
XX XX
XX XX Soybean, anti-influenza, protein, 114-115 amino acids, 12%
XX XX SCN resistance, Rbq1, Rbq4, SCN resistant allele plant breeding
XX XX 249011 region G3; 319013 region A3; 515002 region G2; PCR primer; 88
XX XX
XX XX Glycine max.
XX XX
XX XX M0209151627 A2.
XX XX
XX XX 13 77-7791.
XX XX
XX XX 04 JAN 2001; 2001W0 SE00272.
XX XX

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[illegible]

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PT 24 JAN 2000.
XX
XX PF 28-JUN-2001; 2001MO-1B01477.
XX
XX PR 15-JUL-2000; 2000MS 219704P.
XX
XX GENESET; GENSETT.
XX
XX PI Cohen D, Blumenfeld M, Chumakov I, Abderrahim H, Bihain H.
XX
XX WT, 2000; 15524370.
XX
PT Set of novel map-related biallelic markers, preferably located on
PT density marker-associated chromosomal regions on chromosomes 4, 10
PT and 19, useful, for e.g. detecting statistical correlations between
PT marker allele and a phenotype.
XX
XX PS Example 2; Page 257; 31pp; English.
XX
CC The invention relates to a set of novel map-related biallelic markers,
CC preferably located on density marker-associated chromosomal regions on
CC chromosomes 4, 10 and 19. The markers are useful for genotyping or
CC estimating the frequency of an allele in a population, for detecting an
CC association between a genotype or phenotype and a phenotype such as a
CC disease involving drug responses, obesity disorders related to
CC heredity, such as hypertension, diabetes mellitus, hepatic function
CC disorders, cancer, cardiovascular disease, hypertension, hyperlipidemia,
CC insulin disorders, abnormal glucose tolerance test results, etc. The
CC markers are useful for detecting a statistical correlation between a
CC biallelic marker allele and a phenotype trait or between a biallelic marker
CC allele and a phenotype. This sequence represents a new primer used to
CC amplify a human density-associated biallelic marker.
XX
SC Sequence 18 BF, 7 A, 7 C, 1 G, 3 T, 6 other:
SC
SC Query Match 48 qf, Score 137, FN 24; Length int
SC Best local similarity 83.3%; Pval 1.1e-04;
SC Matches 15, Conservation 0, Mismatches 3; Indels 0; Gaps 0
CY 1 TCCTGACCAATAGTAA 18
CY ||||| ||||| |||||
Db 1 TCCTGACCAATAGTAA 18

```

CC fmo like tyrosine kinase 1 (tk-1), kinase insert domain containing  
 CC receptor (KTR) and/or several other tyrosine kinase (TK) genes.  
 CC angiogenesis, cancer diseases, fibrosis and rheumatoid arthritis) can  
 CC be treated by inhibiting the protein and inhibitor of the expression  
 CC of the protein. Methods for identifying specific examples  
 CC of nucleic acid sequences from the present invention.

XX Sequence 27 BP: 10 A; 3 G; 8 G; 5 G; 1 other;

Query Match: 50.4%; Score 13.9; DB 15; Length 33;  
 Best Local Similarity: 61.9%; Pred. No. 7.3e+03;

Matches 13; Conservative 3; Mismatched 5; Indels 0; Gaps 0.

CC 6 AGCAATACCTAGGACAAAT 26  
 CC 1 AGCAATACCTAGGACAAAT 21

RESULT 16  
 AA57253/3  
 ID AA57253 standard, mRNA, 33 BP.

XX AA57253,

XX 26-JUN-1994 (first entry)

XX Enzymatic RNA molecule 2 kbp RNA target sequence.

XX Specific cleavage; target RNA, protein, Hsp70, Hsp90, Hsp100,  
 XX expression; inhibitor; inhibitor; ribosome; treatment;  
 XX prevention; protein; protein; inflammatory diseases; restenosis;  
 XX cardiovascular condition; hypertension; arthritis; sci.

XX Synthetic.

XX W09402595-A.

XX 03-FEB-1994.

XX 02-JUN-1993; 93WO-0506316.

XX 17-JUN-1992; 9203 0316763.

XX 07-DEC-1992; 9203 0987323.

XX 07-DEC-1992; 9203 0987323.

XX 07-DEC-1992; 9203 0987323.

XX 19-JAN-1993; 9203 0987323.

XX RIBO: RIBOSOME RNAV. INC.

XX Draper KG, Sullivan SW;

XX WPI: 1994-048857/06

XX Enzymatic RNA molecule which cleaves RNA - used for treatment of  
 XX protein; inflammatory; arthritis; rheumatoid; inflammatory diseases;  
 XX or conditions

XX 03-FEB-1994, 7/11, English

XX This is a c-myc RNA target sequence (2.0 kb) which is 75% of an  
 CC enzymatic RNA molecule (ribosome) which cleaves RNA. The  
 CC with the cleavage of the ribosome of a protein. The  
 CC cleavage of the ribosome necessary to effect a therapeutic treatment is  
 CC lower than that of an antisense oligonucleotide and the specificity  
 CC of action is higher.

XX Sequence 33 BP: 5 A; 9 G; 8 G; 11 T; 0 other;

Query Match: 50.4%; Score 13.6; DB 15; Length 33;  
 Best Local Similarity: 60.0%; Pred. No. 7.5e+03;

Matches 13; Conservative 3; Mismatched 4; Indels 0; Gaps 0.

CC 2 CCTGACCAATACCTAAGAA 21

|||||  
 ID AA57253 standard, mRNA, 33 BP.

RESULT 17  
 AA57253/3

ID AA57253 standard, mRNA, 23 BP.

XX AA57253,

XX 06-AUG-2001 (first entry)

XX Canine PCR amplifying forward PCR primer, PCR 27.

XX 3 G; X linked progressive retinal atrophy (XPR), severe retinal  
 XX degeneration, blindness, retinal atrophy, XPR, XPR, XPR, XPR,  
 XX Miniature Schnauzer) PCR primer, ss.

XX Canis familiaris.

XX W0200138578-A1.

XX 31-MAY-2001.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

XX 21 NOV 2000; 2000WO-US31940.

BA (IVME) INVIV NPM JPPPPY  
 XX  
 P1 Madura K;  
 XX  
 DE WFI, 1997 00322/08  
 XX  
 PT Ubiquitin like domains as fusion of localized proteins useful,  
 PT respectively, for assessing the proliferative potential of malignant  
 PT cells or to partly processome complexes  
 XX  
 PS Example 2: Page 29; 94PP, English.  
 XX  
 CC The present PCR primer was used to amplify regions 28 to 328 of DNA  
 CC encoding the yeast PABC protein PABC containing a ubiquitin like domain  
 CC the ubiquitin like domain was a pathway as a major pathway for the intracellular  
 CC degradation of proteins, where the ubiquitin acts as a degradation  
 CC signal. Proteins which bind the proteasome (a multisubunit complex)  
 CC have ubiquitin like (ubli) domain. When the ubli domains are fused to  
 CC a reporter protein, they can be used to assess the proliferative  
 CC potential and select drug resistance of malignant cells. The ubli  
 CC domain also allows the localization of proteasomes for the isolation  
 CC and characterization of novel substrates of the proteasome.  
 XX  
 SC Sequence 17 PP: 15 A, 7 G, 4 C, 4 T, 9 others;  
 Query Match 51.1%; Score 13.4; E: 20; Length 32;  
 Best Local Similarity 72.0%; Pred. No. 6, 1e-03;  
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 CY 1 TCTTGACCAATACCTACGACAA 25  
 |||||  
 DB 7 TCTATGACGACGACCAATACGACA 31  
 RESULT 14  
 AA165664  
 ID AA165664 standard, RNA, 24 BP.  
 XX  
 AC AA165664,  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Primer for studying biallelic polymorphic markers in the IBD1 region.  
 XX  
 KW Human; inflammatory bowel disease; I protein; IBD1; IBDprox;  
 KW intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;  
 KW inflammatory disease; immune disease; cytochrome B; inflammation;  
 KW hematology; liver; cell; T; bcl-2; caspase; caspase; F10 primer; ss;  
 XX  
 OS Homo sapiens.  
 XX  
 FN FR2806739-A1.  
 XX  
 FD 28-SEP-2001.  
 XX  
 PF 27-MAR-2000; ZINC001832.  
 XX  
 PE 27-MAR-2000; ZINC001832.  
 XX  
 PA (DANS) 1. F001. F001. F001. F001.  
 XX  
 PI Hugo JP, Thomas G, Poullet M, Joseph C, Charnillard M;  
 XX  
 DP WFI, 2001 60324/03.  
 XX  
 PT New human nucleic acids associated with intestinal inflammatory  
 PT disease, useful for diagnosis, prognosis and control of these diseases,  
 PT also related proteins  
 XX  
 PS Example 4: Page 47; 97PP, French.  
 XX  
 CY F165664 78 were used to characterize biallelic polymorphic  
 CC markers in the IBD1 gene region. The IBD1 gene encodes an inflammatory

CC bowel disease; I (IBD) polypeptide, which is associated with intestinal  
 CC inflammatory disease. The specification also describes a polypeptide  
 CC which is in proximity to IBD1, and is designated IBDprox. The IBD1  
 CC gene is probably involved in regulation of apoptosis and activation  
 CC of NF-kappa B. The IBD1 and IBDprox polynucleotides are useful as  
 CC source of probes and primers, as source of antisense oligonucleotides,  
 CC for recombinant production of polypeptides, and in screening for  
 CC interactive compounds. The polypeptides are used to raise specific  
 CC antibodies which useful for diagnostic detection or purification  
 CC of IBD1 and IBDprox, to screen for specific binding agents, potential  
 CC therapeutic agents. The IBD1 and IBDprox polynucleotides and  
 CC polypeptides are useful for treatment and prevention of inflammatory  
 CC and/or immune diseases of cancer, where associated with mutations in  
 CC genes encoding IBD1 and IBDprox, especially with mutations in  
 CC inflammatory of the intestinal tract (e.g. Crohn's disease, ulcerative  
 CC disease and Pan syndrome).  
 XX  
 SC Sequence 24 PP: 15 A, 7 G, 4 C, 4 T, 9 others;  
 Query Match 51.1%; Score 13.4; E: 20; Length 32;  
 Best Local Similarity 72.0%; Pred. No. 6, 1e-03;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 CY 1 CCTGACCAATACCTACGACAA 21  
 |||||  
 DB 1 CTTGACCTGACCTACGACAA 20  
 RESULT 15  
 AAX67421  
 ID AAX67421 standard, RNA, 27 BP.  
 XX  
 AC AAX67421;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Human F11 VEGF receptor hamsterhead; k-lyase #147.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; F11;  
 KW F11; F11; hamsterhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumor angiogenesis; psoriasis; rheumatoid arthritis; cancer disease;  
 KW fms-like tyrosine kinase; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss;  
 XX  
 OS Synthetic.  
 XX  
 CS Homo sapiens.  
 XX  
 FN W0015662 A1.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PE 45-OCT-1996; 96W-US1/480.  
 XX  
 PF 11-JAN-1996; 96US-0504040.  
 XX  
 PE 45-OCT-1996; 45US-0009974.  
 XX  
 PA (CHIR) CHIRON CORP.  
 XX  
 PA (RIBO) RIBOZYME PHARM INC.  
 XX  
 PI Eschlebs J, McDowell J, Poullet P, Stinchcomb D;  
 XX  
 DP WFI, 1997 25017/23.  
 XX  
 PT Nucleic acid molecule containing VEGF receptor (F1) for expression of  
 PT RNA stability useful for treating e.g. tumor angiogenesis,  
 PT psoriasis, rheumatoid arthritis, cancer, in a human patient  
 XX  
 PS Claim 9, Page 51; 219PP; English.  
 XX  
 CC The present invention provides for the use of polypeptides which mediate  
 CC the synthesis, expression and/or stability of a cDNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the

